

GAM RNA SEQ	GAM SEQ-ID			SEQUENCED	CHIP_EXPRESSION	CHIP_SIGNAL	CHIP_BG_Z_SCORE
CHIP_MM_Z_SCORE							
TTTGCTGCCTCTCCCAGCTCCC	1	0	2	4807	7.1600103	7.8129125	
CACTAGTAGTCTCTGGC	2	0	1	4435	7.298171	-1.4740227	
GCTAGTGCAGGAAATCTTTGG	3	0	1	2688	13.465069	-4.7450089	
CGCTGCTCCGCCTTGTCCATAT	4	0	1	3421.5	5.0435877	7.0959082	
CCCCACTGTCCCCGGAGCTGGC	5	0	2	65518	22.799175	24.102064	
TGCCCTGGCTCTTCTTGTTC	6	0	2	9983	8.4301682	12.997806	
ACATTCTCTGATTGGTGCCTCC	7	0	2	6695	12.723179	6.4453721	
AATATTTCTTCTAAAGCCCTTT	8	0	1	1018.5	4.8226123	2.7607162	
GTTGAGGTGATGCCAGCCCTGC	9	0	2	3770.5	12.133699	8.0446234	
TCATGGGGCCACAGCTGCCAGC	10	0	1	1294.5	5.4938359	-3.9189341	
TGGGGGACACCAGTCTCTCTCT	11	0	1	3739	4.4848466	-2.4173083	
TGGTCCCCATCCTTGCGATT	12	0	1	4035.5	4.9446163	6.7577944	
TCCTGGGAGGCGGAGGTTGCAG	13	0	2	2269	6.121397	7.7621231	
AGCAAGACCAGGGTTTTGTGTT	14	1	0				
CCCAGGCTGGAGTGTAAATGGTG	15	0	2	3009	7.0731392	13.781642	
AGCCCCTTGGTACTGTCCT	16	0	1	9378	18.433018	1.0831363	
CTCTGTTTGCCTGCTGCCATC	17	0	2	15154	17.421993	10.804789	
GTCTCCCAGCCTACATCTTTCT	18	0	1	7497	5.4792051	-2.7626641	
CCCGGGTGGAGCCTGGGCTGTG	19	1	0				
TCACTGCAAGCTCCACCCTCCG	20	0	2	3370	12.960393	9.7885542	
AACCCAGGAGGTGGAGGTTGTG	21	0	1	2482.5	5.7054992	11.887776	
ACCTTGTGATCCACCTGCTTTG	22	0	2	9350	10.149202	4.1434402	
CCGGCTACTCGGGAGGCTGACG	23	0	1	3014	4.2986312	12.683091	
CTGCCCTGGGGGGCCTCCTTGC	24	0	2	4817	12.989676	3.0056505	
GACCTCATGATCCACCTGCCTT	25	0	2	5103	8.7762318	12.394208	
TTCTCTGTGCTGGGTCTGAGG	26	0	2	5272.5	8.1261625	9.2259359	
TGGGTAGTTTCCCCTGCCCTGC	27	0	1	2944.5	4.1729741	10.251331	
AAAACAGCTTCCTCCAGTGGCTC	28	0	1	2883	4.3991041	8.6778612	
TCACTGCACTCCAGCCTGGGTG	29	0	2	65518	25.576307	20.417265	
CACCAGGAGGACAGGCCCTAC	30	0	1	1419	6.8781896	-4.1960559	
ACGCCTGTAATCCCAGCACTTT	31	0	2	6898	10.893064	18.948416	
TGACCTCCTTTCTCGACTAATT	32	0	2	43651	10.281033	24.914602	
CCTGGCTCTGCCACTTACTGCC	33	0	1	7371	5.4429383	8.8807936	
CTGCTCCCCAGCCTGCGCCTTT	34	0	2	15059	11.630778	16.378119	
CATTGCACTCCAGCCTCCATA	35	0	2	10435	16.077471	9.6274853	
TTCTGATGGTTAAGTTCTGTCA	36	1	0				
CTGCAGTATGAGCTACCCAGGT	37	0	1	671	4.2650108	3.2315347	
TACCATCCAAGCTGGTTTG	38	0	1	1295	5.434535	7.9920983	
TGGTTTCCCTTTTGGCCTCTCC	39	0	2	10935	11.08107	6.0971227	
ACTCTTTCTGCCCACAGG	40	0	1	2806	5.5159893	5.3098421	
GGCTCACTGCAAAGTGTGCCTC	41	0	2	6270	10.347923	7.3339972	
ACCATTGCCCCCTAGTGTCTGT	42	0	2	6005.5	16.011629	9.1782494	
CATTGCACTCCAGCCTGGGTGA	43	0	2	65518	29.090452	30.6901	
TTCTGGTCACTGCTGTTCCCT	44	0	1	6518.5	5.1799512	10.527549	
GTCATGGTGCTAGCGGGAATGT	45	0	2	23180	29.411751	28.092485	
GCGCCTGTGCCTCCTAA	46	0	2	17094	12.760594	23.842529	
GCCCTCCTGGCAGGCAGTGATG	47	0	1	3239.5	4.4799371	8.1225739	
CTGTAATCCCAGCTACCTGGGA	48	0	1	902	4.8697472	5.3667827	

CAAGGGTTTGCATTGGCTTT	49	0	1	2817.5	4.1292181	6.8459005
GTTTCTCTGGGCTTGGCAT	50	0	2	8298	10.689093	5.6611276
CCTGGGAGGCTGAGGCTGCAGT	51	0	1	2965.5	4.9182892	9.9978838
CACTGCAAGCTCCACCTCCCGG	52	0	2	7048	12.263177	14.099768
CACTGCAGCCTCGACTTCCCTG	53	0	1	8874	6.8341184	1.4886127E-2
CCCGGGTTGTCCGCGCGTCCGG	54	0	2	7828	9.6190052	4.963129
TAGCACAGGGCTCCTCAACCCA	55	0	2	1806	7.8335514	5.4125681
TCCTCCCCAAAGCCCAGCCTGG	56	0	1	3388	4.4911599	5.001718
ACAAAGTGCCTCCTTTTAGAGT	57	0	2	65518	13.412503	32.421429
CCCGGGAGGTGGAGCTTGCAGT	58	0	1	2094	5.0106125	8.1183786
CACTGCACTCCAGCCTGGCGAC	59	0	2	65518	21.073904	27.87985
CTGGGCTCAAGTGATCCACCCA	60	0	1	2046	4.3300858	5.4814286
TCTTTGCTATTGTGAATAGTGC	61	0	2	9707	23.491186	2.1807733
GTATGTGCTGAGCTTTCCCGC	62	0	2	2572.5	6.3526735	4.20855
ACAGATTCACTGCACTGGCCAT	63	0	2	15207	9.5306025	12.396938
CACCTGTAATCCCAGCACTTCA	64	0	1	2591	5.442101	10.425298
CCCCTACACACCCCTCTTGGA	65	0	2	13065.5	7.4358983	7.0756011
TCCTTCTCTGTGAGGAGGCC	66	0	2	10471	20.063852	2.295146
CAGGCTGAAGTGCAGTGGTGTG	67	0	2	2136	8.2628632	9.4549208
CGGAGTCTTGCTATGTTGCCCA	68	0	1	1781	5.2067318	5.238801
GCCATCCTGATGACAGGCCACT	69	0	1	3787	14.638888	-0.88807422
GCTCACTGCAACCTCCGCCTTC	70	0	2	42294	20.673286	23.478565
TCAAGCCATTCTCCTGCC	71	0	2	7209.5	8.1129141	18.200718
TATTCCAGCCGCTTGAGCTCGC	72	0	2	4174	10.310376	2.8741286
GCAGCCTGGGCAACAGAGTGAG	73	0	1	2157	4.5432754	10.740927
TCACCAGGCTGGAGTGCAGTGG	74	0	2	4254.5	12.14083	15.720531
TGTGACACTGGCCATCTGGGTT	75	0	2	2784.5	11.518049	11.150477
TGCAATCCCCGCCTCAACAGGA	76	0	2	7725	6.5569119	20.462164
TGCCTGTTGCCACCTGATAAA	77	0	2	5059	6.2758183	2.6550572
TCACTGCAACCTCCACCTTCAG	78	1	0			
TGCGCGCCAGCTCCCAGGTTCCG	79	0	1	2256	5.0988479	6.3105674
GCGGGGTTCCGTGCCCCAGAGT	80	0	2	4053	7.8508492	13.874727
TTGCCAGGCTGGAGTGCAGTG	81	0	2	30880.5	19.972326	29.117062
ACCATTGCACTCTAGCCTGGGC	82	0	2	24856	14.974783	26.093969
CTAGAGTGCAGGTGTATGGTTA	83	0	2	1669	7.7501578	4.8546963
TGTGCTGGCCTTTGGTGACTTC	84	0	2	65518	44.612064	26.016636
GCCCTTTGTGTCTGGCTGGGGT	85	0	2	5320	11.978069	10.261797
GGAGGCGGAGGCTGCAGTGAGC	86	0	2	2820.5	9.8273449	10.098513
AGCTCATTGCAACCTCCGCCTC	87	0	2	30089	17.692238	12.997955
ACTGCACTCCTGCCTGGGTAAAC	88	0	2	46280	12.181033	26.546303
TCGCGGGTTGCACATGGCCATC	89	0	1	3200	5.0210557	12.488149
ATTGCACTCCAGCCTGGGCGAC	90	0	2	65518	24.324524	35.482765
GTGGCCCCAGGGCCCTGTCTGG	91	0	1	2103	4.3064132	5.4394917
GGGCAGATCACCTGAGGTCAGG	92	0	2	3840	11.253606	14.604554
GTCCCCGCCGTGCTCAGGCTG	93	0	1	5861	5.2278342	1.3164479
GGCCCCCGGAACGCTCTGTGACC	94	0	1	8124	16.673124	-2.3175049
CGGTGCAAGGGTAGCGGCAGGC	95	0	1	3417.5	4.6143517	0.71493685
GCTCAAGCCTTCTGCCCACCTC	96	0	1	1983.5	4.2462573	7.6688213
GAGCCCAGGAGTTTGATGCTGC	97	0	1	2802	4.1153555	12.440318
TGAGTCAGCCTTGGCAGCCCCT	98	0	1	4321	9.5403223	-0.46607512

TTTCACCATCTTGGCCAGGCTG	99	0	1	1450.5	5.8872299	6.5283771
GGACACGTGGCTGAAGGCGGCC	100	0	2	3613	11.24597	5.512249
CGGGGTTTCATCCATGCTGTGGC	101	0	1	3762	4.0037775	5.9347458
AGTCCTGGCCTGGGGGACC	102	0	1	4747	5.1204491	11.736219
GCTGCACCCCAGCCTGGGTAAAC	103	0	2	7858	6.2366548	20.271864
ATGCAGCCCCCTGGTGCCCGGG	104	0	2	14258.5	14.995996	10.545995
TTAGGGTTACACCAGCCTCCTG	105	0	2	12631	6.595377	2.2383578
GTGGCTCACGCCTGTAATCCCA	106	0	2	20268	15.527308	18.321419
CCATTGCACTCCATCCTGGGCA	107	0	2	37862.5	18.121622	18.236954
GACCTTGTGATCTGCCTGCCTT	108	0	2	7752	23.901592	13.466584
TGTCCCCACCCAAATCTCATCT	109	0	1	2845.5	5.6470904	0.60507727
ACCTGTCTGCCTCCCACCATCAA	110	0	2	6789	17.796188	8.0814438
GTTGGCCAGGCTGGTCTCAAAC	111	0	2	1993.5	6.2810149	2.2314062
CAGCTGTTTCATTGTTGCCACCC	112	0	1	3205.5	5.7638865	-1.2926182
ATAGCAGCGCTGGCCCTCTGCC	113	0	2	11135.5	8.3489428	16.26886
AGTGGCCTGGAGCCCCGCCTGG	114	0	2	64840	12.445142	20.585953
GGCCGTGAGCCCCGATTTGCCA	115	0	1	3015.5	4.7711444	4.6092601
GCTGACCCCTACAGGTTGTGTT	116	0	2	7867	6.2393546	19.308796
CCTGGCTCCTACGGGTATTTTG	117	0	1	3308	4.5325184	0.97975397
CTCAGCTTGGCCTGGACGTAGC	118	0	1	4410	4.8741584	14.490013
CTCCTTGCCATTTCTTTTC	119	0	2	5430.5	13.120463	6.2777233
CCCAGGAGGCGGAGGTTGCAGT	120	0	2	2787.5	6.7205362	12.188313
CCCAGCAGTAGAGCTCATATGG	121	0	1	4022	20.382507	-2.8780954
TCTCGATCTCCTGACCTTGTA	122	0	2	7138	10.617272	15.065091
CACCATGCCCGGCTAATTTTGG	123	0	2	5040	7.316802	9.882267
TAGCCCTTCTCCACCTCGCCC	124	0	2	8140	13.744523	2.9828069
CCTGTGCTTGGCCAGAGAGGTT	125	0	1	3994	4.3371038	14.052099
CATGCCTGTAATCCCAGCACTT	126	0	2	10382	14.765577	17.657774
CCTGGGCCTCTCAAAGTGCTGG	127	0	2	7478	6.5816064	16.968868
GTCCCCGACGTTTGGCTTGATG	128	0	1	3207	4.4545999	5.6476693
CTGCACTGACTTCCCCGGCTGC	129	0	1	2702	4.0437126	7.0977674
TCCTGGGATCAAGTGATCCTCC	130	0	1	2812	4.0140038	-0.25205359
TTGCTAGTGTTTGGTTGATGGT	131	0	2	13321	29.278065	21.353354
ATCATTATCCTCCTATTTGCCT	132	0	2	2916	8.0566654	5.4937286
TGCTCTGATTTTGGCCAGCT	133	0	2	10768.5	14.230415	7.0602937
TCTGTGTCTCCACCCAAATCTCA	134	0	1	3991.5	4.6330791	-6.5020531E-2
TACTATGGTTATTATCCCTCTCC	135	0	1	1264	4.0216489	1.9981372
GGAGTGCACTGGCGTGATCTCG	136	0	2	3942.5	10.745003	10.263955
TCGAAGGCCTCTTGCTCCTCGA	137	0	1	1306	4.9944282	4.6041131
GTATTTGGAACCAACAGTGCC	138	0	2	1363	7.8097911	4.1715727
TTGCCAGGCTGGAGTGCACTA	139	0	2	11492	11.738238	20.495441
CTGTCCCTGAGCAACTCCTGTT	140	0	2	2516	6.2773986	8.6073799
AGCGTGTTGGGAGGAGCTGCAG	141	0	2	1410	9.0065594	8.8227701
CGGGGCTGGAGTGCAATGGCTC	142	0	2	3585.5	7.393702	15.612262
GGGCGTGGAGCTGGAATGATGT	143	1	0			
GCTGAACGAGCTGGCCAAGTTC	144	0	2	9451	6.6551905	19.321331
CCACTGCACTCCAGCCTGCCAA	145	0	2	65518	20.333113	17.882483
TCTCTAGTCCTGCCTCCCC	146	0	2	12753	19.169752	7.0407801
CACTGCACTGCAGCCTGGAGAC	147	0	1	6050	5.6199274	17.140821
ATGGGGTGAGTGACGCCCTC	148	0	1	1899	5.3449593	1.7462343

AGCACGGTGGGTTTGGCTGGCA	149	0	2	8532	8.91047	7.0811062
ATGCCACTGCACTTCAGCTTGG	150	0	2	7484.5	6.5842552	19.414671
ACATCCTCCCAGATCTACTGGCT	151	0	1	3651	4.4286699	1.3539879
ACTGTCCGGGACAGGCCCATCC	152	0	2	1271	9.39785	2.6795073
TGACAATGAGGCCCTCCACAAA	153	0	1	1679	5.1023388	2.1864455
AAGTGCTAGTGAGTCTATTGTA	154	0	2	15263	30.581371	17.914198
GACCTCGTGATCCGCCTGCTTT	155	0	2	4080.5	7.6009617	13.947659
TGACCTCCTGGGCTCAAGCC	156	0	1	1564.5	4.9039502	-9.6304779
CTCGACTTCCCTGGCTTGCGTGA	157	0	2	6890	6.5380254	11.584653
AGAGATGGGGTTTCACCACGTT	158	0	2	2101.5	7.7702832	10.676204
GGTGGCAGTAGCACTGGGCCTG	159	0	2	1077	6.041307	2.6370835
GTGACCTGGCCGCCTAAACCCA	160	0	1	5941.5	5.6531525	18.527802
AATTGCACGGTATCCATCTGTA	161	0	2	18407	8.3120737	26.950815
CTGTCCTGTGCTTTTTACTGTC	162	0	1	5185	5.3258371	1.2787153
CCTGCCTACTGAGTTTTATATT	163	0	1	3745	12.145576	4.7314309E-2
GCGGCGGCGGTAGCAAAAATGA	164	0	2	65518	27.5298	22.089998
CTGGCCACTGCACCTCTTCCT	165	0	1	3912	5.3084121	3.5621116
TCAGCCTCCTCCACCCCAGAGT	166	0	2	6996.5	14.03341	7.0927162
AGCAGCAGTATCCTTCCCCGGC	167	0	1	3825	4.4749479	9.2136803
CCAGGAGGTGGAGGTTGCGGTG	168	0	2	2398	6.4942522	7.9789319
GGCTGGCCCCATCCAGGCTGGCA	169	0	2	65518	10.117671	10.864906
TGCAGGTTGCTGGTCTGATCTC	170	0	2	8079	24.743416	17.869699
TGGTGCAGCGTGTGGTGGCTCT	171	0	2	4082.5	9.6208868	12.887189
TTGCCTTCCTGCCAGCTTCTG	172	0	2	5405	6.7744174	12.840696
CTCTTTGGTTGGTTCCTGATGC	173	0	2	9661	15.128378	18.743273
TCACCGAGGCTGGAGTGCAAGT	174	0	2	3619	11.230327	15.315854
GCGTCCGGCCTCTCTCGCTCCCG	175	0	1	3319	5.4790416	5.205163
CGGTGCCTCCTCCAGTGTTGCT	176	0	2	8559	10.886886	9.833169
CAGGCTGGAGTGCAAGTGGCGCT	177	0	2	7523	15.30444	19.097713
AGGCACCACATCTCCCTCCCC	178	0	1	2510.5	5.2200365	3.5559428
GATATGGAAGGCCATGCC	179	0	1	1268	6.3048329	0.48396423
TAGAACTATGGCTATGTGCCA	180	0	2	2523.5	18.843672	7.4688845
GTTGCCTAGGCTGGTCTTGAAC	181	0	2	4155	10.291553	9.7640581
AGCACCTCCAGAGCTTGAAGCT	182	0	2	7872	6.2408533	20.331314
GGGTTGGCATCAGGGTTCTGTG	183	0	1	4777	4.5148683	8.4523115
ACTGCACTGCAGCCTGGCCAAC	184	0	2	10584	7.3915148	12.856659
TTCCTGCAACCTCCGCCTCCC	185	0	2	32044.5	19.90851	19.617628
CTCACTGCAACCTCCGTCTCCC	186	0	2	36527.5	21.028955	23.176895
ATATGCAGTCTCTTGCCCTTCT	187	0	2	18270	7.3851495	16.705791
GGCCTGTAATCCCAGCTACTCA	188	0	1	3140.5	5.8857031	12.328485
AGCAGAGTGCCCATCCCGGA	189	0	1	1287	5.9567142	7.4900131
CTCACTGCAAGCTCTGCCTCCA	190	0	2	18388.5	17.632027	21.920879
GTGGTAGCTCCAGGCTGTCTGA	191	0	2	10711	30.533655	22.150589
TGGCGGCGTGTGGACTGAGGAC	192	0	2	15121	9.9330997	18.565649
CCCCTCAGTTTGCTAGTATTTT	193	0	1	11735	24.905746	1.1986766
ACTGCCCTCCAGCCTGGGTGAC	194	0	2	21572	13.925464	26.790289
GTTGGTCTTCATTAAATGCTTT	195	0	2	3499.5	17.153486	5.8892236
AGCTTTGGTTGCCATGATCTGA	196	0	1	1665	5.5821729	10.27639
CATAATTTCTACCAGGGCCATA	197	0	1	886	5.792675	1.0480881
TCCTTGTGCTGAGGGTGTTGCT	198	0	1	2546	5.148253	3.1969757

TCTGGCTTCCCTCTGTTCTGGG	199	0	1	6739	9.2949047	0.96471214
TCCCCCAGGCTGGAGTGCAGTG	200	0	2	7443	15.029393	17.058321
CTTCATCAGCTGGCTTACTGTT	201	0	1	2296.5	4.4541421	-4.1260543
TGCGTTCCAGTTGCTGCCAGGC	202	0	2	5079	11.194171	5.7294831
CCTGGAGGCGGAGGTTGCAGTG	203	0	2	3559.5	8.169879	12.004289
CCTCTGCACCAACCTGTCAAGA	204	0	2	2057.5	11.429537	3.11975
CACTGCAGCCTCCATCTCTGGG	205	0	2	4050	6.9180322	10.574921
GGTGCCCCATCGCGGGTGGCTG	206	0	2	27077	14.316696	22.61035
GCAGGGAACCTGGCTGGGCTTT	207	0	2	16084	7.1124773	22.951672
CCGTCCCCGGTGTCTGCCTGCGC	208	0	2	48514	9.4747534	7.9190497
ATTAGGAGAGTGGGTGCTAAGT	209	1	0			
ACCCAGGCTGGAGTGCAGTGAT	210	0	2	1941.5	7.7255301	11.090164
CACTGCACTCCAGCTTGGGCAA	211	0	2	65518	28.324137	30.232615
CAGAGCTGGCTTCATGGGTGTGC	212	0	2	5653	6.236114	16.840534
TCTTCCTGTCAATGAGAATTAA	213	0	1	3699	5.0892124	3.8346827
GCAGGCGGAGGTTGCAGTGAGC	214	0	1	1579	4.3141651	8.2424784
GTCTTTTGCTAGCCAGAGAGCT	215	0	2	2153	8.0217466	10.245297
CACTGCACTCCAGCCTGGGCAA	216	0	2	65518	31.916103	33.140068
GCCCCCGTAGTAGATGAGGCGC	217	0	2	16235	27.099997	7.9834018
GGTCGCTGTGTAGGTTTCAGCTA	218	0	1	3938.5	5.7133183	2.4790351
TCTGGCTCTGGAGTCCACCTGC	219	0	2	3242.5	6.90412	4.9786406
GACAGCTCCAGCTCCTCCAGGC	220	0	1	1845	4.1900787	8.3998461
TCACTACAACCTCCGCCTCCTG	221	0	2	28515	18.559631	13.999067
ACCCAGGCTGGCGTGCAGTGGC	222	0	1	1413.5	5.045722	6.4478707
CCTGTGGTCCCTGTCTGTGCCT	223	0	2	17748	13.149311	10.342139
ATTGCACTCCAGCCTGGGCAAC	224	0	2	65518	33.306091	35.513947
TCAAGCAATTCTCCTGCCTCGGC	225	0	2	10092.5	16.702658	19.82888
AATGCTGAGTCCTGTGAGTCTT	226	0	1	923	4.3064132	5.5901709
AGTCGCTGTTGGTCGTGGCACT	227	0	2	2426.5	6.5083675	3.8499751
CTGCAAGCTACCCCTAGCATCA	228	0	1	1187	5.359941	7.49787
AGGACCTGTCCCCTGGCCCACT	229	0	2	65518	15.796532	15.770715
GCAGGCATTAGCCCCCATGGCT	230	0	1	2898	5.201571	11.64039
AGGCCAAGAAGGAAGCAGAGG	231	1	0			
CTTCCTGCCTCTCGCCGCCCGC	232	0	2	7982	10.846725	2.7860351
ATTGTTGCCCATGTTTTTATTT	233	1	0			
CTGGCAGGTTATAGAGCTGCCC	234	0	2	1302	7.096612	5.6983724
TCTCCACAGCTGGCCCCCAAGA	235	0	2	19483.5	23.591568	26.742323
GGGTTGGATCCTGGTGGCTGCC	236	0	1	2919	4.99542	-1.0961211
CCTTTTGTCTGCTTGGTTTCG	237	0	1	5359.5	5.4283695	7.2327213
TGGTGCTTGTGGAGCTGGTGCT	238	0	1	6931	22.109066	-15.237776
CAGCCTGCATCATCTGCAGC	239	0	1	1052.5	6.097331	-9.9813395
TCACTGCAATCTCAGCCTCCTG	240	0	2	13609	16.304766	12.973942
TGGGTGGAGCAGGCTGGTGCTT	241	0	1	1915.5	4.7277126	2.129667
CTGAGATAGGACTCTGCTGGCT	242	0	1	3797.5	4.0238738	-0.4093681
GCCTATCTGTCAAATTTCTCTG	243	0	1	2514	5.7133183	-1.7767694
TTCTTCTGCCCCTTGCCCTGACA	244	0	2	10593.5	16.647232	9.2061243
ACTGCACTCCAGCCTGGGCAAC	245	0	2	65518	37.057747	34.517231
TGCCTAGGCTGGAGTGCAATGG	246	0	1	1842	4.9093466	7.6070156
CTGGCCTGGCGCAGTGGCTCAC	247	0	1	3273.5	4.5061736	-1.0821109
CTCCTTCTGGGCCTGGCAGTGG	248	0	2	17180	8.0816298	15.63814

CAAGGTGCCATGCTGGGCGGGG	249	0	2	2339	11.124713	9.2460661
AGTGGGCCGACAGCCCAGGCC	250	0	1	3009	10.806414	-0.20481651
TGCTTATATTTTCATTGGCCCAA	251	0	1	1737	5.1939707	0.85535181
CCAAAGTGCTAGGATTACAGGC	252	0	2	1345	8.5948114	8.4856577
CGGCACTGTAGTCTGGCTGGGA	253	0	2	3297	6.7212648	9.1534166
TGCCGCAAGTACTGCTGCCTGT	254	0	1	1966.5	5.8571658	3.7118392
GATGTCGTGATCCACCCGCCCTT	255	0	2	3425	7.313684	10.200798
CGTGCCACTGCACTCTAGCCTG	256	0	2	27042.5	12.034669	26.515484
CATGGCAGCTCCTCCAGTGTGA	257	0	2	2256.5	6.8781896	5.7773385
GGAATCCTGCCAGCTCTGCCCC	258	0	1	13916	12.002161	2.1075698E-2
CCAGTACGTTGCTCAGCTCCTC	259	0	2	10610.5	11.484417	2.7025924
TGTCTCCCCACTGGTCTTCCAG	260	0	1	7039	5.6089306	15.167439
CTGGCCTAAAAATACAGAACAA	261	0	1	8784.5	6.609952	-0.46130967
CAGGCTCTTCCCTCTGGCCAAG	262	0	2	25089	10.865691	11.601097
ACTCTGGCCATCTTGACCTTG	263	0	1	4235	5.8999434	14.697995
CGGCGAGCGGGACCTGCGCCTG	264	0	2	13179	8.0060148	5.5586901
TGTGCCTGTTCCCACTTTGCCT	265	0	1	2611	5.0901771	2.5660698
CTCACTGCAACCTCCGCCTCCT	266	0	2	62403	22.993574	18.170233
AGGCTCCCTGAATCGCCCGTTC	267	0	1	3782.5	5.0892124	-3.9663608
CTCTGCCTCCCAGGTTCAAGCG	268	0	2	20999.5	17.079414	18.674911
GCTAGTGTTTGCCAGCGTAGCC	269	0	1	825	4.6319594	4.9597144
GGAGTTCAGACCAGACTGGCC	270	0	1	2430	4.3969355	2.4696999
CTCAGCTCATCCACTAAATCCC	271	1	0			
ATTGCACTCCGGCCTGGGTGAC	272	0	2	15397	13.126676	25.123175
CAACATGGTGAAACCCCGTCTC	273	0	2	8706	11.270616	12.27146
GTGCCGACGCTCCAGCACCATCC	274	0	1	1384	5.1635141	3.8417749
ACTGTACTCCAGCCTGGTGGCA	275	0	2	9608.5	7.5143518	22.582787
GTGACAGTGAATCTAGACAGAC	276	1	0			
TCACTGCAACCTCCGCCTGCTG	277	0	2	39092.5	19.973478	20.767599
TCTGCGGTCCCCTTCTCGCCCT	278	0	2	10190	10.797435	8.6208448
CAGGCTGGAGTGACGTGGTGCC	279	0	2	8766	16.20937	18.915073
CCTCTTTCACCGTGCCTGTCCC	280	0	2	8800	16.616077	5.438931
CTGAGCTCACGCCATTCTCCTT	281	0	2	10524	16.186312	18.177279
GGTGATCCACCAGCCTCGGCCT	282	0	2	5029	8.9257526	7.78508
TGACCCCTATATCCTGTTTCTT	283	0	2	6691	6.3185239	5.4931335
ACTTCCCACCCCTCCAG	284	0	1	3259.5	4.1611338	12.380153
CTTTATGAAAACCTGAATTATG	285	0	2	3768	23.111034	14.960108
CGGCTCACTGCAGCTCCGCCTC	286	0	2	14047	17.9716	6.964889
GGCCTGTGGTGCGCTATTTTCA	287	0	1	3159	4.7927871	10.763789
CTTGCTTTCAGTCTCGGCCTCA	288	0	1	1763	4.0555487	1.144424
ATCACTTTGAGTCCAGGAGTTT	289	0	2	7335	6.5335536	19.718058
GAGGCAGAGGTTGCAGTGAGCT	290	0	2	2657	8.4238987	11.530189
CTGGCCAAGATGGTGAAACCCC	291	0	1	29538	10.824452	1.9062781
GCCTGGGTCCACCGCTCGCGCT	292	0	2	7299	6.5360622	9.6849566
GAGGCCACTGTCCCTGCCTTCC	293	0	1	3343.5	4.653738	9.7698135
ACCCGCCGCACGTCCAGGCTGA	294	0	1	5018	5.1787949	-1.1583936
TGGCTTCCCCGGAGTGACATGT	295	0	2	13507.5	16.857716	15.057426
GGAGGAGCATGAGAGGGTAGTG	296	0	1	1193	4.0301342	-18.279354
GCTGTCCAGCCCTTGTTACCT	297	0	1	2068	6.8781896	-1.7931671
GCCTCCAGGTCGGTCTTTCTCT	298	0	2	7529	13.077046	6.7496343

AGGGAAATCTCAGCTCTAAAAT	299	0	2	8991	16.352005	20.399546
CTCAGTGCAACCTCCGCCTACT	300	0	2	4516	8.8905106	13.512998
CCGGTCTGTGTACTTGCTGGCC	301	0	1	10835	16.283325	0.65039492
CACTGTCTTCCTTTGGCTCCTC	302	0	2	8497	10.860129	11.864268
CACTGCACTCCAGCCTGGGAGA	303	0	2	65518	22.925808	34.725494
TACTGTGTGCCAGCCGAGCTG	304	0	1	1632	5.7854853	4.7016063
GCCCAGATCTCCTGACCCTCAG	305	0	1	4383	4.3306851	5.3791971
TCACTTCCCAGACGGGGTGGCA	306	0	1	1907	4.2122374	7.5382385
TGCTGCCCTAAGACCACCTT	307	0	2	4950	11.124713	13.249466
ACACTGATGTTGGCCCTGGTCA	308	0	2	6128	7.7381911	9.9548664
ATGGCTGCCTGGGCGCTGGCCG	309	0	2	65518	12.023874	4.5536995
TTTCTCCTCATGACTGGTTGTG	310	0	1	2943	4.1956687	3.8969367
AAAGCGCTTCCCTTTGGAGCGT	311	0	1	6099	5.6389537	17.599831
AACGCCCAGCCTTGATCAAATG	312	0	1	983	5.3299565	0.62059402
TGAGCACATGCCAGCCCTTCTC	313	0	2	7638	17.835676	6.0798554
GACCTCGTGATCTGCCGGCCTT	314	0	2	2588	16.253777	11.608788
TGGCTAACAAGGTGAAACCCCG	315	0	2	22025	9.0206518	5.915132
TGTGCTCTGACTTTCTCCTGGT	316	0	2	6627	6.2784839	12.047
TCTAGGTAGGCTGTGTGTGGAA	317	0	1	20581	30.987326	-4.863667
GAAGTGTAGTCTTGAGCCCCCA	318	0	1	2564	9.2326555	-0.1792703
CCTGCCTCCCCATCAGTTATACA	319	0	1	7820.5	15.964743	1.1131122
ACCACTGCACTCCAGTCTGGGC	320	0	2	65518	19.886633	30.113441
CTGCTCTGGTTTCCTCTGTC	321	0	2	7506.5	7.7015729	15.622507
GGGGCATTGTGTCTGGGTTCCCT	322	0	1	2912	5.6041431	2.0277293
GCTGGCAGACTTCCTCTGGAAC	323	0	2	1985	9.0118723	2.4699371
CCTCCAACCATAGGTCCAGGGG	324	0	1	1203.5	6.5887036	-0.78580427
TCTCCTGGAGCCCAGATGCTGG	325	0	1	2100.5	4.8226123	5.4119086
CTCCTTGCTGGTCTGGTGTAAAT	326	0	2	12887	13.768332	6.9087734
AAAGTGCTGGTATTACAGGTGT	327	0	2	1430	8.6389112	8.4515057
CTCCAGTTGGCCCCAGTTGGTT	328	0	2	10654	12.255802	17.910707
CCTCACTCAGGTTTGGACCCTG	329	0	2	7301	15.895414	5.3846102
ACTGCACTCCAGCCTTCAG	330	0	2	65518	16.869547	28.85684
TGCCTAGCCAAGTCCAGTATTT	331	0	2	5823	17.976177	16.478537
CGCATGAGACCTGCCGGCCATC	332	0	1	2073	9.8048887	-3.4777019
ATGCCCTGGCCTGGGGAACAT	333	0	1	5475	5.3843775	17.659876
TCTCGCTCTGTGCCCCAGGCTG	334	0	2	8558	11.966861	10.057902
TAGTGCCCTCCCCTTTGGGATA	335	0	2	3843	11.037247	12.832376
GGCTCCTGGGGGTGCTCCTGCC	336	0	2	9895	9.94205	8.883275
AATGGGGTAGTGGGCAGCCTGG	337	0	2	7138	14.468472	13.397085
AACCCAGGAGGCGGAGGTTGTG	338	0	2	3802	7.9819422	12.273234
GGCTCACTGCAACTTCCGCCTC	339	0	2	31704	19.028578	16.190495
CCCGGAGGCAGAGGTTGCAGTG	340	0	1	1643.5	5.8650842	6.6221547
CGCCTGGCCCCCAGTACTTTGT	341	0	2	65518	14.386203	22.674049
TGGCTGTACATTGGAATTATCT	342	0	1	4116	4.8355722	0.55707508
CGTGCGCCTCAGCCTCGTGCGC	343	0	1	3284	4.5142207	12.660418
TCAGAATATGGCTAGGAGTGCT	344	0	2	1830	9.6709318	10.3449
CAGGCTGGAGTGCAGTGGGGCG	345	0	2	4013	11.398844	15.757032
TACGCCTGTAATCCCAGCACTT	346	0	2	5888.5	12.35752	15.497684
TGTCCTTGCAAATAACAT	347	0	1	1509.5	5.3898416	8.1098919
CTTCCCCAGGCTGGTCTGTAT	348	0	1	3686	4.3019638	-0.81996107

CATGTTGGTGTGCTGCACCCGT	349	0	2	3866	8.1607409	11.896873
AGGCTGTAGTGCATGTGCTATG	350	0	2	17379.5	8.1088619	26.406704
ACTGCGCTCCAGCCTGGGTGAC	351	0	2	46098	18.273163	32.816708
AGTCCCCCTCTGAGCCCAGGGA	352	0	1	5483	5.3878217	-0.95005888
TAGGTATAGGATTCTAGGTTGG	353	0	2	1295	6.1877456	2.5713561
CAATCCCAGCTGCCGGGCTGC	354	0	2	7442	8.735631	7.0616617
CCATCCCTTGGAAGCTGGTTTTA	355	0	2	4197	11.864914	11.215641
GTGCTCCCTCCTTCCTCAAGGA	356	0	2	3789	7.298171	9.6469736
CCAAAGTGCTAGGATTACAGGT	357	0	1	1054	4.3064132	4.0962029
TGGATTCACACCATTCTCCTGC	358	0	2	7131.5	8.6853085	6.5294394
AAGTGCTGGGATTACAGGCATG	359	0	2	1812	7.3370275	10.102645
TGAGATGGAGTCTCGCTCTGTT	360	0	1	1785	5.1520457	7.9560995
TTGCTGCTCTGCCGGTACAGCT	361	0	2	9885	6.0708628	22.70689
GCCTGTCCCGCACCGGAGCCCG	362	0	2	2397	7.096612	10.159995
GTCTCCCCAGGGCCCTCTTCAT	363	0	1	4158	6.0783563	1.3304862
TGGATGGCTGTGGTCTTTGCC	364	0	1	4573	7.9280648	-2.8086965
CTTCCTTCTCACTAGCAGCGCC	365	0	1	2665	5.1787534	2.627044
TCCTTTGCTTCTGTCAATTCTCC	366	0	1	2483	4.0944448	6.7577206E-2
GAGGCTGAGGTTGCAGTGAGCT	367	0	2	1999	6.8439331	8.8330622
GTAATATGTGCTGAGTCCT	368	0	1	1202	4.4296627	8.1321344
CTGGTTATCTCGGCCACAGAGA	369	0	1	3187.5	5.22434	-0.64146328
GGCCACTGCTCTCCAGCCTGGG	370	0	2	40431	15.478172	22.089659
CCTGGCTCTGGCTTCCTGTTGT	371	0	2	34525	11.373339	6.4300051
AGCCCCAAACACCAGGATTACT	372	0	1	4319	8.0879526	1.9557818
CCGCCGCTGATAGCTCTGGGC	373	0	2	7166	6.0192232	10.085858
AGGGGCTCCTTTGTGCTGCGTC	374	0	2	1911.5	7.5021071	5.5356297
TCTTCACGCCAAGTGCCCTCA	375	0	1	4150	9.149087	-6.0181384
GGCCTCAGTGATGATGGGTTAAA	376	0	2	6124	6.4003	5.4322863
AAGGCTCGGCAATGTGCGGCTC	377	0	2	1617	6.3867145	5.1396852
TTTCCCTTTAGCCTGAGAATCC	378	0	1	2392	5.359941	11.933125
CAAAGTGCTAGGATTATAGGTG	379	0	2	1570.5	9.1333447	8.6484661
GAGGCAGGAGGATTGCTTGAGC	380	0	2	11218	8.9163761	23.396725
TCCGGGTGCCACGTGCCCTA	381	0	2	13959	8.1505041	9.7457113
GAGGCTGAGGCGGATGGATCAC	382	0	2	37381	14.008185	28.093838
ACCACCCAGCCAGCTTCTCCCT	383	0	1	6121	8.7047195	-0.78491044
TGTCCAGCCGGCCACGCCCAT	384	0	1	2478	9.9760656	-5.2396908
GGCTCTTCGCCACCAGCCACA	385	0	1	1624	4.4541421	1.0276202
TGCAGCATTGCACTCCAGCCTG	386	0	2	11232	11.505449	21.076042
TGGGTCTCTGGCCACCCAGCC	387	0	2	12948.5	8.0436459	19.699574
TCTCTAGTCTCCTTTAACCTGA	388	0	1	1148	5.2546234	2.501446
TAGGTTGTCCATCTCTAGAAGC	389	0	2	1004.5	8.2524061	4.2505751
ACTGCAGTCTTGATCTCCTGGGC	390	0	1	4871	4.5565634	1.9227443
ACATCTAGACTCTTGCCCTCTT	391	0	2	6310	10.886886	15.850095
CTGGTCTGCCACCCACACCCCT	392	0	1	5580	7.5570545	-1.1313673
GTGCCAGGCACAGGAAGCAGCC	393	0	1	1855	4.0386124	0.18331024
TCCTCCCTCACCTCAGTCTGGG	394	0	2	8976.5	11.361602	9.0995693
GTCTCACTGGCCGCACGCTGA	395	0	2	8536	7.1346483	19.281561
CTGGCCTCGGCAGCAGGAACAG	396	0	1	3757	4.0009317	4.5684352
GAGTGCAGTGGCGTGATCTCTG	397	0	2	1660.5	6.5337977	5.7436481
GTGTTCTGTGCTGGATGGTCA	398	0	2	2131	11.864914	6.3784571

CCAGGCTGGAGTATAGTGGCGC	399	0	1	1270	4.4945917	7.4746661
CCAGACCCTCCATTCAAGCTCC	400	0	2	8423	9.3362026	7.7677507
CACTAGGCTGGAGTGCAGTGGC	401	0	2	4301	12.202009	16.549067
TCACTGCGCTTCAGCCTGGGTG	402	0	1	1929.5	5.0829325	1.1913716
TCTTTGCTATTGTGAGTAGTGC	403	0	1	3427	15.098435	-1.562425
TTGTATAGCCCAGAGAGTGAGA	404	0	2	1038.5	6.9170618	6.1502376
CATTGCACTCCAGCCTGGGCCA	405	0	2	65518	29.033922	21.707558
CTGCCCCGACCATCCCCGGGCT	406	0	1	1967	5.5675011	7.4003267
CGGCATGGGCGTCCCCCTCACT	407	0	1	6042	5.6168065	9.6102333
TTGCATTTGGTTCTGCCTGGTA	408	0	2	7111	6.8737931	11.158542
GAGCCCCACCCTAGACATTCTG	409	0	1	2592	5.6915727	-3.6630919
GGATGGACGTGATGCCTTAGCCA	410	0	1	5225	18.121622	-2.3604157
TGCCTGCTGTATTCCAGAG	411	0	1	1491	5.1635141	7.662797
CCTGGTCGGCGTGGTGACGGCG	412	0	2	6434.5	6.2044091	6.2762375
TCACTGCAGCCTCTGCCTCCCG	413	0	2	17181	17.958405	9.3027229
ACTGTACTCCAGCCTTGCGGAC	414	0	1	3187	4.4324884	14.526779
CTCCAGTCTTCTCATGTATCCC	415	0	1	2943.5	5.1170878	6.0549593
TAGCAGTGTCTAGGTAGGCCAT	416	0	1	7447	24.057808	1.1526781
GCCCTTGGCCTCTTTGGCCCGG	417	0	1	6460	6.3274021	-0.69839072
CATTCTGCGATCCTCAAGCACA	418	0	1	1481	4.0957041	9.367939
AGCAGCTTTCACCTCCCCGCCT	419	0	1	65518	12.03591	0
TGGAGCCAGCGGCCTGCTGAGG	420	0	1	744	4.4214902	3.8499751
AGCTGGGGCTGTGGTTGTGATT	421	0	1	3007	5.3449593	10.225232
TAGCTGAGCCGCCTGGCTGGGG	422	0	2	9026	6.8317003	8.4015751
CCATCACCTAACTAGTG	423	0	1	2735.5	11.982088	-3.3107362
GCCTGGCCTAATTCCAGCATTT	424	0	2	62842.5	13.758234	31.293688
CACAGCCTCCTCTGGCTCACGG	425	0	2	14804	7.7305474	23.87908
CCGAGGTCCTGGACTTGGCCCT	426	0	1	6198	7.1988444	-1.3169746
GCAGAGTGCTGTCTGACGCCCC	427	0	1	1421	4.527245	1.0200601
CTGTAAGTGTCCCTTTTGCC	428	0	1	3318	4.9795561	11.643893
TCACTGCAACCTCCACCTCCTG	429	1	2	45662	20.504339	18.911047
TTGCTTTGCAGTGCCTATAGGA	430	0	2	1273	6.826138	5.0606236
TGGAGGCTGGAGTGCAGTGGCG	431	0	2	2034.5	7.5323806	10.788618
AAGGTGGAGGTTGCAGTGAGCT	432	0	2	4275.5	9.1417122	11.853789
GCAGGCTGTCTAAAGTTAGAGT	433	0	1	960	5.3449593	4.6880941
GCGCCCCATCTACAGTACTTTT	434	0	1	3901	7.4468746	1.8634913
TCTGCCTTCTATCTTTTGTCTG	435	0	1	2195	4.2943249	5.856668
CCTTCCCATGCAGCCTGTCTGA	436	0	1	4066	5.3572183	6.7426419
GCCTGGCCTAAATTAGTAATTT	437	0	2	65518	14.47023	33.939186
TTCTGGCTTCTCCCAGGCGGCC	438	0	2	5582	8.2352791	10.879703
GGCGCCCCCTTCAAACAGAGCA	439	0	1	1745	4.7277126	8.7167349
TCCAATAGCCTAAGAGCCTGG	440	0	1	2742.5	4.4703951	1.2259418
GCCTGGCCAACGTGGTGAAACC	441	0	1	18181.5	9.7641363	-0.38965413
TGTCTGGCTTTCTTCAGTTAGC	442	0	2	6191	9.9906111	15.989508
TGGGTTTTGTTTGTACAGTGTA	443	1	0			
CTGTGGTGAGGCCCTAGAATCTG	444	0	2	3222	11.085442	6.6749387
TTGCTCAGGCTGGCGTGCAATG	445	0	2	9724	11.115126	19.742767
GGAGGTGGAGGTTGCAGTGAGC	446	0	2	4936	10.584228	13.28014
GGAGGCGGAGGTTGCAGTGAGT	447	0	2	2351	7.6334682	8.3588333
CTGAGCCTCCTGCTTCTATTTT	448	0	1	1864	5.9849868	3.7265418

ACTGTACTCCAGCCTGGGAAAC	449	0	1	4692	5.6260824	17.568949
TCACATTTTCAAAAGCTGGTGAC	450	0	1	764.5	4.7752681	-3.7142565
CGCACCCCACTGTCCCTCAACC	451	0	2	4601.5	6.5281987	4.8853817
ACACTTTGCCCCCTGGCCGCTT	452	0	2	42189	12.009233	22.436626
GCAACTGAACATGTGTGTGGCC	453	0	1	2167	6.7475801	0.27415401
CCCAGGAGTTGGAGGCTGCAGT	454	0	2	4273.5	6.2922449	14.155445
GTCTGTTTTCTCTTCTGTGGGA	455	0	1	3260	4.4957891	12.91537
ATGGTACTCCAGCCTGGGTGAC	456	0	2	4173	7.3957338	16.409479
AGAATCCCAGGCCCCACTG	457	0	2	3122	8.3376312	13.851473
ACTGCACTCCAGCCTGGGTGAC	458	0	2	65518	27.343826	34.911034
TGGTAGGTTGGGCAGTTC	459	0	2	8731.5	31.377066	20.530041
CAGCCCTCCTACCCTGCCAGGC	460	0	2	7825	9.6958656	6.1267514
AGTGAGCAAGTTGATAATGGCC	461	0	1	2206	12.457526	1.2831149
CCCTGCCTGTCCTGGTCCCGTT	462	0	2	18466	9.747386	21.814604
CACTGCTACCTCTGCCTCCCGG	463	0	2	19159	17.182699	10.042536
GCTGTGGAAGTCTTTATA	464	0	1	1228	5.2394924	0.15779255
TCTGAGCCAGGGTCTCCTCCCT	465	0	2	2987	6.3731112	9.5772123
AGGAAAAAATTAATGTGAGTC	466	1	0			
ATTGCACTCCAGCCTGGGTGAC	467	0	2	60365.5	24.984217	35.201714
GCCTGTGTCTGGGTGGCCAGAG	468	0	1	3356	4.7288775	1.1448419
TGTCCTCGTCCGCCTCGAACTC	469	0	1	2812.5	4.2049069	-1.0601429
CACTGCACTCCAGCACTCCAGC	470	0	2	6054.5	6.051445	10.920486
GGTCTTTTCTGCTGCAGGTTGT	471	0	1	3605	4.629807	6.2433772
GGAGCCGCGGCCCTTCATT	472	0	2	4182	6.2263575	9.809968
TTTGGTGTTCGGTTCATTGCTG	473	0	1	1967	4.1357851	5.2781134
GAACTTGTGATCCGCCCACCTT	474	0	1	2483	4.4610376	7.0900927
CTTCTGGCTGGTCAAGGACT	475	0	2	4005	8.6937799	9.6446276
GTCAGTCATTGAATGCTGGCCT	476	0	2	8592.5	23.067156	11.230301
GGAGTTTGCCTATTGCTTTTGG	477	0	2	3720	6.173347	6.482801
CAGGCTGGAGTGCAATGACGCC	478	0	2	2761	6.4190331	12.467172
CTCTGATGTCTGCCCCTCACCT	479	0	2	12084	23.231821	2.7038672
AAGCCCTGGACGGCCCTTCCCC	480	0	1	4492	7.5995965	-3.6259129
GACCCTCTAGATGGAAGCACTG	481	0	1	3638	4.4202566	13.507792
CTGGCCAGATGTTACGTCCAAT	482	0	1	2339.5	9.680912	-11.645831
AGCTGGTTTAATATGCTGTCTG	483	0	2	11390	14.25641	8.7015753
TCCTGCCTGGGGCCGCCTG	484	0	1	2616	4.7310023	10.146957
GAGCTGGGCCTGCGAGTGCTGC	485	0	1	2060.5	5.0099111	1.7965864
ACGCCCAGACTCCCATACTTTG	486	0	1	2459	4.50102	4.1521502
TTAAAGCCTCCCTCATAAGGA	487	0	2	3650	8.3206406	14.328845
CCCAGGGGTTCAAGGCTGCAGT	488	0	1	1033	4.0216489	6.0328941
TTCCAGTTCTGGGCTGGCTGCT	489	0	1	3769.5	4.0091105	3.8919213
TCTCTTCCTCCGCGCCGCGC	490	0	2	7111	6.0010505	12.012436
CGTGACTGGGTCCGTCTGGCT	491	0	1	4430	5.1234531	8.6597939
AACCCGGGAGGCGGAGGTTGTG	492	0	1	1833	5.103756	10.290462
GGCCCCGCAGACCCAGCACGT	493	0	2	1905.5	6.5486112	6.9167981
ACTGTACTCCAACCTGGGCAAC	494	0	1	6841	5.909749	20.226805
CGCCCGCTGGCCCTGCGATCTC	495	0	2	65518	15.196337	33.776985
CTCACCTCCAGGAGCTGCTGGC	496	0	1	8262.5	9.149087	-4.4073544
ATGGCCCTAATGAGTTGGTGTT	497	0	2	5385.5	19.2614	5.6697388
GGTAGTCGGCCTTGCCCTGGGC	498	0	1	1782	5.1635141	8.7292385

CTCGCCCCTCTCAGCCCTGCAA	499	0	1	14248.5	19.352268	1.4588933
GCCCCAGCTCACCGGCTCACTG	500	0	2	15345	20.667051	7.4258513
AAGTGCTCATAGTGCAGGTAGT	501	0	2	27166.5	9.1624584	28.31859
CAACTCACTGCGGCCTCAACCT	502	0	1	3783	5.4047599	5.8278494
CCTCTTCAGGCACTCGAAGGCC	503	0	1	2775.5	11.314644	-1.779775
CTGCCATGCCACTGTGACTGCA	504	0	1	2352.5	10.038951	-0.80460918
CCCAGGCCCTGGCAGAGCTTGT	505	0	1	3205	4.2292862	11.181579
TGCAGAAACAAGCCATCATTCA	506	0	2	1094	6.8781896	4.4873405
GGCTCAATGCAACTTCTGCCTC	507	0	2	6445	11.169347	10.793466
ATTGTACTCCAGCCTGGGTGAC	508	0	2	13270	12.799824	24.968328
CTGGGAGGCAGAGGTTGCAGTG	509	0	2	1910	6.9613633	10.357609
GCAGCTGACATCTGGCTGGGCC	510	0	2	2573	8.120388	3.4149001
GTCCAGTTGTATGTCCAGTGTC	511	0	2	2058	8.4334011	5.2194672
TGACTACAACCTCCACCTCCCG	512	0	2	4496	8.9163761	9.9170055
AGGCTGGAGTGCAGTTGCATGA	513	0	1	1154	4.7976661	6.3405333
CACCTGGCTGGCAATTTATAAT	514	0	2	9852	8.0965796	17.484594
GCTCCCTGGTAGCCATGCTCTC	515	0	2	12312	6.6286459	3.9085872
CTAGACTGAAGCTCCTTGAGGA	516	1	0			
GAGAAATATGGCTCAGTTCCAC	517	0	1	1451.5	5.3449593	6.0128675
CTCACTGCAAGCTCCACCTCTT	518	0	2	4183.5	15.744108	13.408605
TCACCTTGTGATCCGCCACCT	519	0	1	2944	5.0713305	4.4200244
ACTGCACTCCAGCCTGGGTAAAC	520	0	2	65518	29.763027	35.404873
ACTGCACTCCAACCTGGGTGAC	521	0	2	5289.5	9.2819481	17.745958
TTCCTGGTCTATTTAGAATTGC	522	0	1	3974	4.2977972	7.7437348
CTCGTGATCCGCCACCTCAGC	523	0	2	9254	12.490854	15.083214
CACTGCACTCCAGCCTGCGCAA	524	0	2	65518	26.453463	34.462708
ACAATGCTCCCTGTAGTCAGGA	525	0	1	1874	4.6958904	7.40031
AGGAGGCCCTGGCGTTT	526	0	2	7670	9.8578186	18.796598
ACTGCACTCCAGCCTGGGT	527	0	2	65518	27.764378	33.832714
CTCACAGTCTGCCTTTCCCTTG	528	0	2	4450.5	6.7386289	12.351869
TCTCTCTTTTTTGAACCCGCTC	529	0	1	2311.5	4.0555487	1.0858992
AAATGTGGGGCTGGAGGCAGGA	530	0	1	4164	4.2210102	16.645317
CAAGCCATTCTCCTGCCTCAGC	531	0	2	18892	18.51676	21.383736
CCTGCCCTGCTCACTGTCGGTA	532	0	1	4583	4.9649172	0.75725234
TGCACCACTGCACTCCAGCCTG	533	0	2	65518	25.040926	34.867786
GGCCCTGGTCCTAGGGGTGGAA	534	0	1	3918	5.2506523	-11.347021
CACGCCTGTAATCCCAGCACTT	535	0	2	13062	15.57386	18.50495
ACTTGGAACCTGGCCCCTTTCAT	536	0	2	17782	14.512917	23.881441
CAGGAAAAGGCGGCTCGGGGCT	537	0	2	27684.5	9.7338009	6.1309323
TCGCCAGGCTGGAGTGCAGTG	538	0	2	16241	17.047142	24.279329
GTGGCCCATCACGTTTCGCCTT	539	0	2	65518	14.54515	20.760025
CAAGTGATCCTCCCATCTTGGC	540	0	1	2388	5.3808784	7.4311776
GAGAGGTGGAGGTTGCAGTGAG	541	0	2	2534.5	6.4362307	12.629781
TTTCCCAGCCTCAGCTCAGCAG	542	0	1	4894.5	7.2876582	-0.72574896
GTGCGGCCTGGCCTTCAAGTGG	543	0	2	15350	9.6908836	19.487803
CACTGCACTCCAGCCTGGGTCA	544	0	2	65518	26.882214	33.427895
ACCTCCTGGCCTCAAGCAATCC	545	0	2	58457	12.381654	19.294073
TGGGAGGCCAAGGCAGGCGGAT	546	0	1	1193	4.9847255	7.2392049
TGTCCTTCTTGTCTTGCCCAA	547	0	1	3592.5	5.1910453	1.0036907
CCCGGGAGGTGGAGGTTGCAGT	548	0	2	2962	7.343236	13.058587

GCCACTGAGCCCGGCCATTGTT	549	0	2	2514	7.7381911	2.2476037
GTCTCGGACTCCTGATCTCAGG	550	0	1	1380	4.1414785	3.9894354
CAGGAGGATTGCTTGAGGCCAG	551	0	2	9887.5	8.4761457	19.047802
AACCCGTGATCCTGACTCCCCT	552	0	1	7080	5.843668	7.8386455
GCTCCTGGCCGGGCTGCTCCTG	553	0	2	27106	14.495318	9.280777
AAGGGAATGTTGTGGCTGGTTT	554	0	2	3896	10.519875	13.251223
ACCATCTCCTGTGCCTCCAGCT	555	0	2	16520	12.522655	19.197701
TCTGCCTAGAAACAGTGTTTGC	556	0	2	5275	7.7571926	3.0926366
TTGGTCCCCTTCAACCAGCTAC	557	0	2	20228	9.5504265	23.87529
GCCTGCTCCCAGTTGGCGCCTC	558	0	1	3775	7.6600766	-1.6529437
CGGGCAAGGCGAGACTAGGCC	559	0	1	1455.5	5.7638865	-0.9456889
GGGGGGCGCCATGGTCTCTTGG	560	0	1	3867.5	4.3061237	-0.1289482
ATGCCACTGCACTCCAGCCTAG	561	0	2	49924.5	14.368088	30.30353
GGTCTGTCTTCCCAATCGTGGC	562	0	1	4046.5	4.2799697	6.4598308
GGCTGTGGAGCTGCAGAGTTGG	563	0	2	5971	7.1055961	2.2149129
CAGGCTGGAGTGCAGTGGCGCC	564	0	2	4637	11.871922	16.185398
GGCCCCTCTGAGCTTACTCTGT	565	0	2	6262.5	11.684633	9.8594589
GCGCCTCCTCGGCCTC	566	0	2	12734	7.9515629	6.2195482
CACCAGGCTGGAGTGCAGTGGC	567	0	2	5291	13.367915	17.112989
TGGCTAGGCTGGTGTCAAGCTC	568	0	2	2082	6.3935094	7.687212
GCCCAGCCACAGTCACTTTCAT	569	0	1	2139	4.7320642	8.6496077
CTTCCCACCATCTCCTG	570	0	1	2625	4.8619056	7.170155
GACCTCAGGTGATCTGC	571	0	2	5069	10.007993	16.466791
TTCCCTGGGACTGGCCTGCACC	572	0	2	17948.5	9.3010607	15.061718
ATGTTCATATCCCCATTCTGAT	573	0	2	1760	8.5004892	7.7344885
CATTGCACTCTAGCCT	574	0	1	875	4.0046587	2.2476213
TCACTGCAACCTCCACCTCCCA	575	1	0			
GCCATTTACACAGACATTTG	576	0	2	1978.5	6.6882792	9.8837452
GTAGTCCCAGCTACCCCGGAGG	577	0	2	3868.5	12.13766	12.272501
CCTGTCATATACATACCTCCTC	578	0	1	1712	4.1733551	4.783987
TCTCTCAGGCTGGAGTGCAGTG	579	0	2	2711	9.6044931	12.843214
TAGCTACCATTATTGAGCACCT	580	0	1	757	4.2067757	2.5492058
GTTTACTTGTGCCTTGGCTTAA	581	0	1	1948.5	4.0322022	-15.512288
AGCGCCGCCCTGCTGGTGTG	582	0	1	4465	4.3703461	6.2275581
TCCAGGGCCATCTCCATGAGGC	583	0	1	1948	5.4790416	9.0826721
TCAGTCTTGAACAGCCCCCTGT	584	0	2	6402	12.333841	7.9963231
ACTGCAACCTCCACCTCCTGGG	585	0	2	26924	17.396763	10.658098
TGGTGGAGGCGCTGCTGGCCAG	586	0	2	11424	10.211181	12.62489
CTGCAGCCTTTGCCTCCTGGGTT	587	0	2	8429	12.857187	13.758839
GGCTCACTGCAACCTCTGCCTC	588	0	2	62440	23.696358	18.67169
TGCCGAGGCTGGAGTGCAGTGG	589	0	2	2467.5	8.8668938	8.8795528
CCGGGTTGAGGTTCCCATAGAT	590	0	2	6920	8.8808632	18.126587
CTGCTGCGCTGGCCGTACGGT	591	0	2	45168	18.758972	18.507338
TCCTGGTCTTCAGGTTGCAAAA	592	0	1	7121	5.3691082	9.0031843
CACCCTCAGCTCCCGGGGGCT	593	0	2	5651.5	10.5429	4.3305707
CATTGCACTCCAGCCTGGGCAA	594	0	2	65518	32.881447	28.077059
TCAGGGGTTGGCTTGTGTGTT	595	0	2	20519.5	8.8405285	21.048086
AGCCTCTGGTCCTTTTTTCCCT	596	0	2	11308.5	12.165344	5.3993454
ACTGCACTCCAGCCTCGGGGTC	597	0	2	49031.5	14.262467	31.189104
GCCAGCCTCCATCCTCCCTTG	598	0	2	10191	21.391727	11.342846

GCTCCGCCACGCCCACTCCTAC	599	0	2	4705	6.8716969	9.635397
CCGCGGGGTCATGGCTGGGCCG	600	0	2	7300.5	6.5837302	5.0417223
ATGGCCCTCTTATCACAGCTCC	601	0	2	5586.5	21.480997	6.3762493
AACCTTGTGATCCACCCACCTT	602	0	2	3034	7.7903786	12.639959
CAAAGGGAAAAGCCATGTGGGC	603	0	1	1205.5	6.3321967	-1.1940883
TCCTGGCTTGTACATCTACGT	604	0	1	4198	4.4526401	3.8407443
CATTGCACTCCTGCCTGGGCAA	605	0	2	65518	27.010284	16.583426
GGCCTCTTATCTGGCTCCTGCA	606	0	2	5318	6.4274201	6.5868769
AGTGGCGTGATCTCGGCTCGGT	607	0	2	3395	8.8775339	14.742507
TGGCTATTCTTGGACACA	608	0	1	2806	18.035503	-3.2833591E-2
GCTCCCCAAAAGCTCCAGGAAA	609	0	1	2161	5.5307322	0.0302024
CCAGGAGGTTGAGGCTGCAGTG	610	0	2	5379	11.585869	13.504684
ACAGCCTCCATCTCCTGGGCT	611	0	2	5043	8.2979441	10.987616
CCAGGAGGCGGAGGTTGCAGCG	612	0	1	1831	4.9563489	9.9608593
TGCCCGGATACCCCTGGCCTC	613	0	2	46111	13.316625	10.030684
TGCGACCCTAGCCCCCTCACTT	614	0	2	5417	11.129067	4.3243365
CTGTCCTGGGGAAAGCCAGCCC	615	0	2	1892	8.5004892	5.7830157
GCAGCTCCTGGAGGTGAGAGGCG	616	0	2	5368	7.8018293	15.956004
CACCCAGGCTGGAGTGCAGTGG	617	0	2	4215	12.088334	14.940107
AGCCCTCGTTTCTGCATCCTGT	618	0	1	4923	15.10443	0.58649576
ATTGCACTTCAGCCTGGGTGAC	619	0	2	11488.5	11.742085	23.617636
TCTTCTATCCTCAGCCCCTGCC	620	0	1	5352.5	9.7554712	1.239718
GTGGCTCACACCTGTAATCCCA	621	0	2	15446	13.370042	20.396935
CACTGCAAGCTCCGCCTCCTGG	622	0	2	16781	17.735508	9.1570225
GTGGCAGACCTTCCCTTCTCCT	623	0	2	4139	6.9686718	8.4107714
GCTCACTGCAACCTCCACCTCC	624	0	2	33649	18.60092	20.711613
TCTAAGAGAAAGGAAGTTCAGA	625	1	0			
TTGTTCTTGTCTTTGCCTTCAC	626	0	1	4146	5.8114853	5.746397
CCAGGCTGGAGTGCAGTGGCAC	627	0	2	14590	15.059402	24.507948
AAAGTGCTTCCTTTTTGAGGGT	628	0	1	4403.5	4.8706794	7.6543956
TCCAAATGAGCTCTGCCTTCCA	629	0	1	8231	5.6790619	11.278896
GCCTGTAATCCCAGCACTTTGT	630	0	2	6291	12.232025	12.874677
AATGTGTTGAATAAATTGTGCC	631	0	2	1493	7.7202153	3.8070927
CCAGCCCGAATCCCTGGCCAGG	632	0	1	3382	13.906728	1.8086184
CTAGATAACTTATTTTCAAGGA	633	0	1	693.5	4.0893412	1.9033302
GCTGCTGGGCCATTTGTTGG	634	0	1	4101	7.4591732	1.3319389
CTCATTGCCCAGATCCCCACAG	635	0	1	2016	4.838347	8.3423147
CTGTGGTACAGCTGGGACGGA	636	0	1	664	4.6319594	3.5137784
GTGTTGTCGCTGGGTTTTGAGGG	637	0	1	3030	4.5279474	3.9595523
TGGAGTTGGCTGCAGATGAGTC	638	0	2	9954	13.087917	15.585505
CAGTCACAAGCGTACCTAATTT	639	0	2	2097.5	9.4896584	6.2945709
ACTGCAAAGGGAAGCCCTTTCT	640	0	2	14213	7.6344547	19.22015
AGCGCCACTGCACTCCAGCCTG	641	0	2	65518	21.477427	32.126575
CACTGCACTCCAGCCTCGGTGA	642	0	2	65518	19.946772	34.137524
GGGCTAGCCTCTTCCCTGCTCC	643	0	1	2982	4.0539145	1.5543098
TGCGCCATGTGCTCTCGGCCCT	644	0	1	3290	5.4790416	8.9091539
TTTTGGCCACATCCTTTTGAGT	645	0	1	932	4.3311777	5.6849165
CGGCATCCCCACTTCCTCCTGC	646	0	2	5467	7.7441764	4.2301731
CTGGCTCTCAGGCTGGTCCCCA	647	0	2	11103	17.197889	7.7209744
TGCACCACTGCACCCAGTCTG	648	0	2	5009	7.3463378	16.848854

TGCCAGTATCCTTCTGAGACCC	649	0	2	9374.5	18.697142	19.309006
GCAAGTGTCTGTCCCCTT	650	0	1	2829.5	5.2069716	4.7231493
TGACATTTCTAGTGCTTTGTG	651	0	2	1338.5	7.1093221	8.5563574
TCAGTGCAGTCCAGCCTGGGCA	652	0	2	65518	34.101166	18.829176
AAGACCAGCCTATGTTTTCCAT	653	0	2	1307	6.3594904	4.4498701
CTTAGAGATGGGTTTTACTTAG	654	0	1	886	7.7022095	1.8901725
AAAGTGCTGGGATTACAGGCAT	655	0	1	1350	5.680541	7.7369747
CTGGCCCCCTTTCATTCTGGAAG	656	0	2	11008.5	19.356289	14.29258
GCCTCATTTCACCTCCCC	657	0	1	7161.5	19.507957	0.16928124
TTCCCTGCCATACCTGAAGGCA	658	0	2	3785	7.4591732	4.4417677
GGTTTTATCCTACCCACACAGC	659	0	1	2980.5	5.771091	0.75884527
TGCGCCTGGGGCCCTGGCTGTC	660	0	1	4313	4.8216996	7.0607853
CACTGCACTCCATCCTGGGAAA	661	0	2	6397.5	6.6049953	18.619169
CAGTTCCTCCGCCAGCACTTC	662	0	2	6955	6.4068542	9.6022158
CCAGACCATTTTGCCTTACC	663	0	2	38076	30.955603	11.095823
TACAACCTCTGCCTCCCAAGTT	664	0	2	6090	14.013508	12.263943
CGCCATGTCCAGCGTCTTCGGG	665	0	2	8765	20.334946	20.485155
TGCCTCCAACAGCCCATCCTAG	666	0	2	5709	13.713832	8.2213135
TCACCAGGCTAGAGTGCAGTGG	667	0	1	1159.5	4.8244257	6.5572648
CCCACTGCTGCGCCGGGCGCCG	668	0	2	17950	21.138054	12.695562
GCAGGCTCTGGCTTATTCTGGG	669	0	1	4399	4.4706116	13.904231
GCGCCGCCATCCGCATCCTCGT	670	0	2	4801	16.34218	9.281786
TCACATCTAATTCCATTTCTGC	671	0	2	8429	13.263923	4.5787411
GTGACACCCGCATGCCACTGTG	672	0	1	4433	5.2274818	8.4032717
TGCAGCCTCTTGTTTCAGCCCC	673	0	2	11243	15.895414	2.5227482
GGCCCAGTGCAAGCTCTTTCTG	674	0	2	2960	7.6298795	6.4523926
AGGCTGGAGTGCAGTGGTGTGA	675	0	2	7407.5	15.261675	13.995954
GCTCACTGCAAGCTCTGCCTCC	676	0	2	20572.5	19.847269	12.887133
CAAATTCCATTTCATGCTCCCTT	677	0	2	3158.5	7.6177769	5.7730742
GCCATCCCAAGCATTTTGG	678	0	2	3676	17.232298	13.983404
GACAAGCTCCCGGTGGCCCTCC	679	0	1	12851	9.4387512	-5.8295474
AGCTACCTGATCCTTCTTCTGA	680	0	1	3226	4.1367669	12.153009
GGGTAAATCTCTTTTCATGGCT	681	0	1	3221	4.827455	8.7138081
CTGTCCTTCCAGCCGAAATCTA	682	0	1	2360	4.3559012	11.170581
GCATGGCTTCGGGGTGCTGCCT	683	0	1	3747	5.1863647	12.211168
TAGGACCCTGGTGGCCCCC	684	0	2	5109	8.5892859	8.0437737
AAAAGGGACGACAACAGGCCAC	685	0	1	1681	4.7831736	-0.22445607
CCCAGCTCTTCAAGTCACCCCC	686	0	1	2752.5	5.4642267	3.5884585
ACTGCACTCCAGCCTGGGACAC	687	0	2	65518	25.933289	35.343163
AGCTGGCTTACTTGAGATGCAT	688	0	2	3049	8.8567095	7.4132333
GACCTTGTGATCCCCCTGCCTT	689	0	2	6915	8.0644264	17.640575
CCGCCTGGCCCATTGCAGGGCA	690	0	2	65518	18.506096	29.045151
TGAACTCCTGACCTCATGATCC	691	0	2	6999.5	26.17539	18.849899
GACCATCCTGGCCAACGTGGTA	692	0	1	3690	4.9752827	15.844102
CCCAGGCTTTTCTCTTGCCCCA	693	0	2	5771	12.212635	10.303027
TTCTTCAGCCTACCTTGACCTC	694	0	1	1982	4.5595746	0.49319306
CTGCGGGGCCTGGACAGGGAGG	695	0	2	11797	7.1950088	21.891239
GGCTGTGTGGCCGTGGGCTCTA	696	0	1	1700	4.3887382	4.3097105
GGGCCACCCCCTGCCCACGCT	697	0	1	3459	4.6319594	4.3550696
CCCCACTGTTTTCTTCATCCTA	698	0	2	50957	31.882698	4.8442335

GGAGTGCAGTGGCGTGAGCTCG	699	0	1	1283.5	4.7879038	3.6301775
TAGGAGGATTGCTTGTGGCCAG	700	0	1	3154.5	4.6519237	4.9273152
CTGAGGGCAGGTGGTGTGCCA	701	0	2	1847.5	8.3489428	5.0725312
GCACCACCACCATCGGCACCTC	702	0	2	3012	6.4477148	2.4866204
CTTGTTTATCTCTGTAGCCCTG	703	0	1	3684	5.9854388	8.3862486
GTGGGTTTCGTGGTCTCGCTGGC	704	0	2	65518	26.617212	17.195196
AAAGCCCTGGCCAGACACCAGT	705	0	2	5732.5	6.8473902	6.6282077
ATCGGCAAGCCCCACACCGTCC	706	0	1	1713	4.0142264	9.0132332
AGCCTCAGGTTGTTGGTTCTT	707	0	1	1042.5	4.1900787	4.8052392
CGGTGGGTGCTTCAGGCGGTGG	708	0	1	3999	5.0099111	5.715847
AATGGTCTTCCTCCACCCCTCTG	709	0	1	4451	4.8959856	5.1994057
TCACTGCAAGCTCTGCCTTCCG	710	0	2	9055	7.7008362	11.763208
TGGTCTTTGTCCCTCCTTGATC	711	0	1	3743	4.256711	2.9960811
AGTGCAATGGCGTGATCTTGGC	712	0	2	5951	8.6127348	17.549313
ATGCCACTGCGCTCCAGCCTGG	713	0	2	44255	14.692498	32.195774
TTTCTTCCTGCTTTGTCCCATG	714	0	1	4054	5.4825935	11.238956
CTCTCGCCAGCGGGGCTGCGCT	715	0	2	13140	7.6419506	17.506365
TATGTTTGGCCTGGCAATTTCA	716	0	1	2780	4.5881057	9.7094517
CCACCAGCTGCATATGCACGTA	717	0	1	1730	4.4214902	1.1879559
GTGTCCCCACCCAAATCTCATC	718	0	1	2826	5.9052849	6.1014419
GGAAAGGCCTGGGTGTCTGGG	719	0	1	5274	6.3618565	-1.7002298
GGGCGGATCATTGAGGTCAGG	720	0	2	1943.5	6.9547186	9.5280085
ACTGTACTCCAGCCTCGGTGAC	721	0	1	3141	5.0527177	14.756032
GATAATCCACTCTGCTGACTTT	722	0	1	3054	4.3317614	6.3779197
GCCTGTAATCCCAGCACTTTGG	723	0	2	8675.5	12.842025	14.392535
TTTAAATCACAACCTCTGCCCT	724	0	2	15129	15.825633	8.2785378
GATGAGTTTGCCTGGCCTGCAG	725	0	2	25445.5	12.297516	17.035336
TGCCACCCCGGACCCCGAAGTG	726	0	1	2106	4.6232533	7.5721364
CACTGCAACCTCCGCCTCCTGG	727	0	2	55476	22.094246	10.714499
CACTGCAAGCAAGCTCCGCCTC	728	0	1	7633	15.721508	0.38197863
GGCTCATATCCCGGCCATCATT	729	0	2	2692.5	14.02678	7.6887875
ATTCTGTGCTAACTGCAGGCCA	730	0	2	4140	19.305922	11.530575
CAGGCTGGAGTTCAGTGGTGTG	731	0	1	1648.5	4.3088479	8.9180403
CATTCCTGGCCCGGGCGCCGTC	732	0	1	2736	4.0554576	10.724096
CAGGTTCAAGCGATTCTCCTGC	733	0	2	9179	16.397514	14.266402
GCCTGGCCGGGTCTTGGATTTT	734	0	1	5031.5	5.5863533	7.3384004
GGTTCTCAGCCTGAGCCGCCCC	735	0	1	18192	21.105703	1.4826102
CGCGAGGTGGAGGTTGCAGTGA	736	0	2	2801	7.2209163	4.0311246
TCACTGCACTTCAGCTTGGGCA	737	0	2	31458	10.144489	22.4685
AAGTGCTGGGATTACAGGCGTG	738	0	2	3421	6.6648126	13.608858
ATGTGAGTGCTATGATAGACAG	739	0	2	1139	8.0798817	5.4914975
ATCACCCAGGCTGGAGTGCAGT	740	0	2	4395.5	12.324327	14.314183
TATCGAGCTGGACGGGCTGGTC	741	0	1	6607	5.2088056	6.9531446
GCTGTTTTCCCATAGCTGGTCA	742	0	2	7061	19.803032	6.222959
GGAGTGCAATGGCTTGATCTTG	743	0	1	5693	6.7378373	1.033795
AGGATCTTGCTATGTTGGCCAG	744	0	2	2784	10.949057	7.9714575
CTTTTCCCCTTTGGACTC	745	0	1	4238.5	5.1553736	7.0349116
CTGAGGCTGGAGTGCAGTGGTG	746	0	2	4514	12.474048	16.694977
GCCATGACTCTCCATAACCAAAG	747	0	2	1592	6.0272546	8.5714464
CCTGCTGGCTCTGTTGCTCGGC	748	0	1	13366.5	10.797435	-3.9057117

CCCTGCCTTGTCTGGGCTAGGT	749	0	1	2002	4.0046587	9.0806446
GGCCCAGGTTGGAGTGCAGTGA	750	0	2	2994	8.0930119	10.374014
TGCTCTGTTGGCTTCTTTTGTC	751	0	2	8407	17.417171	17.734081
AGTGATTCTCCTGCCTCAGCCT	752	0	2	35041	21.798445	19.430222
AGTTGGCACTGAGCTGTGATTG	753	0	1	3303	4.4303179	-1.0004215
AAGGTGGGTGGATCACGAGGTC	754	0	2	1791	6.7066569	9.7404299
GAATCCCTTGCAATTATCCCTTT	755	0	2	2882	6.153091	4.2042389
TCCCCAAGCAGGCAATCTCCCG	756	0	1	3149	4.4257097	6.5767608
TGCCCCACTGCTGGCCACCACCC	757	0	2	32112	15.630626	16.785101
GCCCTGCCCTCTCGGCACTCGC	758	0	1	2717	5.5086098	11.520112
AAAGTGCTAGGATTACAGGTGT	759	0	1	820	4.1482205	4.6776071
GGGCGGATCACCTGAGGTCAGG	760	0	2	7018	13.621652	16.918211
CTGTGCTCTTTCCACGGCCCCA	761	0	2	6477.5	13.662484	9.3280506
CTCCCCAGCCCTGGTATTCTGA	762	0	1	5384.5	5.0192461	5.6187172
CATTGCACTCCAGCCTGGGTAA	763	0	2	65518	31.334749	27.271093
GCGCTGCGCCTCCTCTTCCGCA	764	0	1	2221	4.0475416	8.1211281
AGTGCTGGGCTATCTACTGCTA	765	0	2	18896.5	8.3062468	21.32906
TGTGACTGGTTGTCGCGCTTTC	766	0	1	2849	5.792357	8.2097464
CTCATTGCAACCTCCGCCTCCC	767	0	2	33077	19.544933	20.350861
GCCATTGCACTCCAGCCTAGGC	768	0	2	5526	10.291553	17.393818
TTCCACATGTTAGCTGGTTAAA	769	0	2	2748	17.300783	11.944987
GACTGTGGGGAAGCAGATGCCA	770	0	1	1511	4.0386124	-0.97461921
TGTCGCTGGCCTTCTGGAT	771	0	1	4401	5.2269702	12.950581
ACTGCATTCCAGCCTGGGCAAC	772	0	2	65518	24.732506	33.288292
TCCATTGGCCTTTTATCCTAGA	773	0	2	5760	15.329782	8.1126537
CACTGCAAGCTCCGCCTCTGGG	774	0	2	7054.5	14.676391	11.85893
CTTGGGAGGCAGAGGTTGCAGT	775	0	1	1287.5	5.3808784	8.0099583
TCCACAAGGCAGCTCCTCCAGG	776	0	1	2706	5.4716368	1.7482823
GCTCCACCGCCGCTATGGGTA	777	0	1	3502	4.3559012	3.5113876
CTCGCATGCCCTGCCTCATCCA	778	0	1	2410.5	5.5748396	0.29925746
GGCCGGGGCCTGCTCGCCTGTG	779	0	1	3488	5.4115729	-8.3415947
GGTCAGGAGCCCTTGGCCCCCT	780	0	2	5270	7.1600103	6.9067311
TGGTCTGGCCACATGGTC	781	0	2	8349	13.022524	4.8629713
GGTTCAGAGCCTGCCAGTATA	782	0	1	1813	6.9879608	-2.6342282
CATTGGCCTTTTATCCTAGAGG	783	0	2	4983.5	15.452302	15.902376
TCCTCAGCTTGGCCACGGAGTT	784	0	1	6478.5	5.8972673	17.989834
ATGTTGGCCAGGCTGGTCTTGA	785	0	2	2519	7.2414885	7.5854573
GTCCACAGCTCTGAGGTCTCCC	786	0	1	6493	5.3572183	1.3877324
GCCTAGTGGAATTGAAGGGCC	787	0	2	2352	11.945862	8.8114462
TCAGCTCCTACCCCGGCCCCAG	788	0	2	8279.5	11.228731	17.399603
AGAGTCTCCCTGTGTTGCCCTG	789	0	2	10467	7.4270558	12.602409
GTGTAAGAACCTTCTAGAGCCC	790	0	2	3204	7.0456204	2.6366203
ACTGTAACCTCAAACCTCCTGGG	791	0	1	6067.5	5.62674	11.00416
GTGGCCAACCTGGCCCTGAACT	792	0	1	4379	4.9676137	-1.203916
TATTTGTCTGGTCTAAGGAGGG	793	0	1	3219.5	4.6818242	11.217502
GGAGTGCAGTGGCGTGATCTCA	794	0	2	2509	9.1686945	10.351524
TCCTCCAGAGCTTCATCCTGCC	795	0	2	16927	19.618345	5.2284846
TGAGGCCACCTTGGCCCCGGC	796	0	1	4794	5.7001333	14.264636
ATGATGGCTAGGCTGGTTTTGA	797	0	1	1068	4.3558846	3.1461418
CGCCCCGGACGTCTGACCAAAC	798	0	2	7410	6.9984522	2.8285146

GGCCGCCCTTTCCACGGTTTCT	799	0	2	2520	9.4387512	10.455907
AGGCTTACAGCAGCAGGC	800	0	1	1484	4.7118134	-0.64998931
GGCTTCCTGCCTCGGGCTGGCC	801	0	2	58372	11.079018	4.4936109
GATGGGTTTGTGGAGAGGTC	802	0	1	5425.5	4.8749881	17.533426
TCAGTCAACCTCCACCTCCCG	803	1	2	31810	20.186802	16.772465
GAATGTGTACTGAGTGCCCCTT	804	0	1	5542	12.220497	-4.4586358
TCCACTGTCCCTGGCACTTTT	805	0	2	9134	6.4327211	12.8872
GCACCACTACACTCCAGCCTGG	806	0	2	3563	6.3702331	11.491977
ATGGTAGCTGTCCACATCAGGA	807	0	2	8208	25.85717	21.352978
CTGAGGCAGGCAGATCACTTGA	808	0	1	1210	4.8558879	3.7993965
GTGGCCCAGGTTGGAGTGCAGT	809	0	2	4915	12.333922	6.7368903
GACCTTGTGATCTGCCACCTT	810	0	2	8467	31.729177	18.925035
GTGATCTGCCAGCCTCAGCCTC	811	0	2	7194	15.083432	9.3042612
AGACAGGGTGATCGCTTGAGCC	812	0	1	3466	4.6497626	7.744925
CCCAGGAGGTCAAGGCTGCAGT	813	0	2	2036.5	6.6226544	11.643046
CGGTCTCCCGTGTGTGTGCGCT	814	0	1	4407	5.3256574	16.37768
AGCGGGGTGTTTTGGGTGGCCT	815	0	1	4033.5	8.2409916	0.52406603
GTCTCCTCCCTTTTCATTACCT	816	0	2	4807	8.0566654	3.426122
CCTGCTCTCTGTTCTTAAGCTT	817	0	2	5021	9.0648565	7.4354005
CAAGTGGAATGCTCTTCCTCCC	818	0	1	3123.5	4.0142264	6.7150235
AAGGCCGCCCTTCATGCTCCT	819	0	2	6358.5	9.1175785	8.5895061
TGTCCTCATCCTCCAGTCTGTC	820	0	1	3129	5.6114564	1.2281151
TGGCGATGGTCATTTTTTC	821	0	2	2609	7.1536875	3.1643765
TTGGGGGAGGCCTGCTGCCCAT	822	0	2	3549	9.3567915	8.3044834
GCGGGGCCCGGACCCAGCCTCT	823	0	1	4254	4.2667646	3.5057929
TGGGGTATCCGTTAGTAAGATG	824	0	1	3380.5	4.0906634	13.235014
TGGAGTTGGCCGCCCGGACCGA	825	0	2	8187	7.0123053	19.997877
AGTGTGTTGTAGGCTCAAATGG	826	0	1	1296.5	5.0562248	4.8389935
CGCTTCAGAGTAAGGCGCTGC	827	0	1	2448	4.256711	-0.95797318
GATATCATTGAGCCCAGGAGTT	828	0	1	3794	4.876976	13.768772
CACTGCACTCCAGCTTGGGTGA	829	0	2	65518	18.826578	34.620605
CTGAAGCCCAGCTTCC	830	0	1	10934	14.751002	-0.56149203
CATCTCTGGCTTGGATTATGGT	831	0	1	2875.5	4.1804218	9.7742558
TTTACCTTTGTGGGTCTCCCTC	832	0	1	3593	4.5381126	8.0754824
CTAGCCCCTACTCCAAGTTGA	833	0	2	6032.5	13.43356	13.731526
GCTGGCAAGGTGCTGGAGGGCC	834	0	2	3498.5	14.638888	3.7599447
TTCCAAAGGCTGCACCTTGCCC	835	0	1	6400	14.44299	-2.3250175
GAAGGGGGAAGAGAGCTGGCCG	836	0	2	63993	20.677708	18.040138
TTGTTCTATCTGCCTCCTGC	837	0	2	4838.5	9.8048887	4.8166785
TGGAGCTGGGTCTGGGGCA	838	0	2	6426	15.46969	17.843594
CACTGCACTCCAGCCTGGGTGA	839	0	2	65518	28.667358	32.660065
CATTGCACTCTAGCCTGGGTGA	840	0	2	20339	14.318895	21.095203
AGCCTGTCCCTTCTCCTG	841	0	2	4545	14.269382	3.7745585
TCACCCAGGCTGGAGTGTAGTG	842	0	2	4518.5	12.479655	15.868072
CTGCTGCCGGAGACTCGTC	843	0	1	1437	4.8540587	2.4149714
AAAACCTAAGCCAGTAGCTCCC	844	0	1	2386.5	4.5235443	0.87618637
GGCTCACTGCAACCTCCACCTC	845	0	2	38975.5	20.41017	17.418346
CTGTAATCCCAGCTACTCGGGA	846	0	1	2806	5.0527177	13.475494
GCCATCATATCCCCTGTGACCT	847	0	2	5493	17.421993	9.6620798
CCAGGTTGGAGTTCAGTGGCGC	848	0	1	1854.5	4.1551623	4.9337268

TGGTTAACTTCTGAGCAGGCTG	849	0	1	1338	4.0301342	2.5747242
GCTGGCTGACAGATTTGGGGTG	850	0	1	3232	5.4790416	-2.1113901
CATCCCTGTCGTCAAGTCTCTG	851	0	1	6284	5.1015582	-0.33885518
AAAGTGCTGCGACATTTGAGCG	852	0	2	20430.5	8.490345	28.331139
ATGTCATGAGGCTAGCCCCCAA	853	0	1	1710	6.4409542	-1.0215437
AATCACTTGAACCCAAGAAGTG	854	1	0			
TGAGGCAGGCGGATCACGAGGTC	855	0	2	1475	6.1789246	8.965416
AAGAGGTAGCAGTCACAAAAGA	856	0	1	682	4.1900787	3.1956244
CCGTGGTCACCTGAGCTCCTTG	857	0	1	2997	4.0277519	-1.3587624
CAGTTTCTTCTCCCCCAGAGA	858	0	1	2348	4.165566	0.71364939
ATCTTTTATCACTCCCCTGCT	859	0	1	5396	5.4679914	11.567021
TCACCCAGGCTGGAGTGCAGTG	860	0	2	6851	14.545588	17.889225
TCTCCAGGCAGGAGTGCAGTG	861	0	2	2795	6.2941146	8.1798553
GGGGCTGGTCTTTCCACTTACT	862	0	2	65518	11.24554	19.391401
TGTAATCCCAGCTACTCGGGAG	863	0	2	4677	11.408354	16.218851
CTGATCTCAAGTGATCCACCCA	864	0	2	2249	7.9458203	9.493042
TAGGTTACAGCCAGCCAG	865	0	2	1963	10.949057	11.221157
CCTCTGTGTCTCCAAGAGGCCT	866	0	1	3752	9.7851496	0.61701149
CTGCCTGCCTGGCCCAGGAACC	867	0	2	65518	14.752467	36.164337
ACAAAGTGCCTCCCTTTAGAGT	868	0	2	65518	22.461653	34.028076
GGGGAAAGCCAGCCCTGCTTCC	869	0	2	1892.5	6.826138	6.2401505
GGAGTGCAGTGGTGGGATCTCA	870	0	1	1541	5.5753407	8.2118359
ATCGATCCCGCGTAAGGCCCCG	871	0	1	1231	4.8226123	1.2662603
TCTGTGCTAGGCAGCCTGGCCC	872	0	2	11107	23.362293	13.677877
CTGTCCCCACCCAAATCTCATC	873	0	2	2917	10.575051	6.3207545
GAGCCGCCCTCCACGATGTCCC	874	0	2	7252	8.6663809	14.735928
GGTGGTGGAGCGGGGCCAGGCC	875	0	2	4320.5	7.4591732	12.328825
TCACTGCAACCTCCACCAGCCT	876	1	0			
CTGTCCTGCCAGTCCTGGACTC	877	0	1	3377	5.8142152	7.2265315
GGCGGGCAGCGTCTTGCTGGCC	878	0	1	4755	7.4653172	-11.274526
TCCTGGGGCTTGTCGCTGGCCA	879	0	2	28926	9.8624611	7.4913173
CAGCTGGTGCTTGCTGGCTAA	880	0	2	7373	13.676201	7.9258513
CAGGCTGGCTCCCTGAAGGTTT	881	0	2	8459.5	6.1472831	17.683357
AGGTGGCCACAAGGTGGCTGGC	882	0	2	13621	20.378857	17.680929
TGGAGACACAGGACCAGACTGC	883	0	2	2004	6.981535	2.3005965
GGCTCTGGCTTTGGAGGAGCAG	884	0	2	4483.5	6.8781896	14.473881
CTGGCTAAGATCCAAGAAAGGC	885	0	2	5036	14.178236	6.6532001
GCTGTAGTGAATGGCCGCGTTC	886	0	2	15429	7.8280811	7.1725068
TGTTTGTGTGGGGCCTTGGC	887	0	2	7702	6.3522415	7.8300943
ATCAAGAGCACAGTGCTGGCAT	888	0	1	1172	4.3064132	2.099376
CTGGGAGGCGGAGGTTGCAGTG	889	0	2	4850	10.57113	16.432323
TCACTGCAACCTCCGCCTCCCG	890	0	2	42376	20.906567	16.209127
TCTCTATTTGCCTAGGCTTGTC	891	0	1	1775	4.0386124	5.2510257
GTGGCGTGATCTCGGCTCACTG	892	0	2	5379.5	9.6190071	14.266473
TCGTTACCATAGCCTTGTCCT	893	0	2	2169	6.6286459	10.14022
CCCAGGAGGCCTGCCTGGCCGG	894	0	1	4711	5.0298901	9.8042231
CAGCTCGGGCCTCCCTCTCCCG	895	0	2	5136	8.3545942	10.162696
ATGAGATGAGGAATGGCCCTCC	896	0	2	2753	10.024472	4.1300974
AGGCCGAGGCGGGCGGATCACC	897	0	1	1354	5.2067318	8.9456701
ACGGTGCAGCCTGTCCCTTCTC	898	0	1	3755	6.826138	-1.7736735

GGAGGTACTGTAGCTGGCGTT	899	0	2	1877	10.634505	9.6884193
CTTTGGAACACCCAGCTCTGTG	900	0	1	4367	4.3228598	8.8246651
TGGGCGACAGAGCAAGACTCCG	901	0	2	8120.5	7.6260972	20.824087
TGGGTGACAGAGCAAGACTCTG	902	0	1	3917.5	4.9988604	13.126308
TGGCTTTAGTAATAAGTTTCTC	903	0	2	12660	16.773508	11.141039
TGCTAGCTGCCCCGAAGGTCTCA	904	0	2	39989	47.058292	15.67876
GCTTCAGAGAGGGGTGAAGCTG	905	0	2	21900	17.158428	13.963737
GCTGCCTTGCCCTCTTCCCATA	906	0	2	8045	13.299488	9.9672127
GCTGTAAGTCACCTGGCCCCGAT	907	0	2	26191	8.8471966	25.053482
TGCTGGCTATCCTGCGCCTTTC	908	0	2	7903	10.469044	13.746831
CCAGGCTGGAGTGCAAGCAGCA	909	0	2	8552.5	10.636292	19.600433
GCTAGGTTGGGGAAGTTCTCCT	910	0	2	2180	6.2453051	9.2986526
CCAAAGTGCTGGGATTACAGGC	911	0	1	2212.5	5.0945106	7.6044312
GCCTGGACTGTTCTACCATTTT	912	0	1	2709.5	4.8429475	1.7205493
GCCGGGCCCGGGTTGGCCG	913	0	2	11714	7.709898	8.2685728
CAGCCTCTATGCCCCCGTCAACC	914	0	2	9484	16.652414	11.957335
CTGGCTAGATGTGTGGCCATGA	915	0	2	3221	21.032122	14.058989
ACTGCACTCCATCCTGGGCAAC	916	0	2	46281.5	15.235478	33.271416
CCTTCTCAGCCCCAGCTCCCGC	917	0	1	3674	6.026938	0.30380982
GTCTCCCAAACCTCTGATGGTCC	918	0	1	5069	6.4115953	-0.19100553
GGTCCCCCATGGTGAGCACTG	919	0	1	2640	6.9299874	-3.5790675
CGGGTTCACGCCATTCTCCTGC	920	0	2	25205.5	15.182484	6.2870688
AGCGACACCGCCTGCAGGCCAT	921	0	1	3210	17.247011	1.8362232
GAACTTGGCCTGTCTGTCTGGC	922	0	1	3174	4.165082	-0.96377498
TGGGTCAGAGGGAAAGTGTAT	923	0	1	1240	5.4864416	4.4304075
TGTTGCCCAGGTTCTCTCCTGC	924	0	1	2527	4.6479778	4.8975463
CATTGCACTCCAGTCTGGGCCA	925	0	2	20401.5	20.588572	15.621833
TGGTTCTTCGCTGGGCGGCTGC	926	0	2	18451	17.683105	11.562138
CAAAGTGCTAGGATTACAGGCG	927	0	2	1593	7.9515629	8.8260517
TGGTAGGTACTGGCTTCAGGC	928	0	1	1959	5.7638865	10.948694
CACTGCACTCCAGCTCTGGGT	929	0	2	65518	20.15584	31.571056
GTCTTGTCCTCAGCTCTGCCACT	930	0	1	5667	5.9998269	10.289277
GCCTGGGAGTTGCGATCTGCCCCG	931	0	2	65518	31.678772	9.6128397
GCAGCATCCCGGCCTCCACTGT	932	0	2	5995	7.2606683	11.881517
TCTGCCCCAGCCGCACTG	933	0	1	3479	5.2319188	7.0148258
ACCCATCCAGTGTCCCTGCTAG	934	0	2	3030	8.7047195	5.2593546
GCCTGGCCAACATAGTGGGACC	935	0	2	16749	8.6138811	20.486101
CATTGCACTCTAGTCTGGGTGA	936	0	1	2023	4.2580843	8.942131
AAGACACCAGTGGCAGCCCC	937	0	2	3888.5	10.940197	2.9559026
TCCTGGGCTTTGGCTTGTTGGG	938	0	2	10813.5	7.7058806	7.1675959
TGGTAGTCGGCCTCGGTGGCTC	939	0	2	38277.5	43.447659	21.633255
TACTGCGCCTTCACCAAGCGGC	940	0	2	2073	6.069356	2.6888943
TCACTGCAAGCTCCGCCTTCCG	941	0	2	11075	17.517977	5.425684
AGTGCCCTTCAGATTTGCCCCAG	942	0	1	5977	9.7207422	0.54957581
ACCCTCTTGAGGGAAGCACTTT	943	0	2	7337	6.0748458	18.790304
GCCCCAAGTCCCTATGTTTCCA	944	0	1	8950	12.678107	1.0439761
ATCCCCCTGTATCTGGAAGAAT	945	0	1	2318	5.7854853	3.7798862
GTGCTTTGCTGGAATCGAGGAA	946	0	2	1710	10.403996	8.5636625
GAGGCTGAGGTTGCAGTGAGCC	947	0	1	1366.5	5.0199966	6.459177
TGGTCGGGCTGCATCTTCCGGC	948	0	2	4093	7.5570545	2.1106353

ACCACTGCCTCCAAGGTTTCAG	949	0	2	3247.5	10.014809	6.09551
TTTGGTCCCCTTCAACCAGCTA	950	0	2	13310	7.6353297	18.880299
GGTATGCTGAAGCCAGCTCGCA	951	0	2	792	6.1946688	4.135592
TTGCTTGGGCTGGAGTGCAATG	952	0	1	2486	4.9725943	-2.7821193
TATCTATGTGCTCTGACCTCTC	953	0	2	6670	9.7406015	7.9747272
AGGAGAAGCCAAGTTGTGAGCA	954	0	2	6905.5	29.559206	20.101482
ACCCATGGTCTGGTGGGGCCCT	955	0	1	4897	5.121223	1.2881944
ACCCCGCTCCTTGACGCTCTG	956	0	2	9609	6.7912097	4.80404
CACTGCAAGCTCCGCCTCCCGG	957	0	2	13890	17.77289	14.108605
ATTCTTGGATTTGGCTCTAGTG	958	0	1	2081	5.359941	9.4660416
ACTGCACTCCATCCAGCCTGGC	959	0	2	5668	7.6480083	10.938603
GCCAGGCTGGAGTGCAGTGGT	960	0	2	12883	15.701074	24.210485
CTGCGTTCTGCCTGGCGGCCTA	961	0	2	5047	6.173347	11.160098
TACTGCAAGCTCCACCTCCCG	962	0	2	9843	15.895414	13.694772
CACTGCCTTGGCCACCTATCCT	963	0	2	10671	9.1234684	14.108407
TCCTTTAAACAACCAGCTCTCA	964	0	1	2428	5.5528088	7.3969135
GGCCTCTCTTGGGACAGCTGTC	965	0	2	2816.5	11.840509	11.64073
GAAGAGTGGTTATCCCTGCTGT	966	0	1	2580	4.6407037	10.335828
CCCTGATAGCCCCTATCATCAG	967	0	2	3127	14.184772	3.5698271
CACTGCAACCTCTGCCTCCTGG	968	0	2	53207	22.508492	13.233194
TCATTGCAACCTCCTCCTGGGT	969	0	2	5648	10.772061	9.7537737
CTGCAGTCTACCTGGATTTTTA	970	0	1	4922	4.5788498	17.83988
GGACCCTAGAGAGAGCCAGCCT	971	0	1	1774.5	10.895789	0.5640983
ACCCGATGTTGGTGCTCTAGTA	972	0	1	2346	5.8714437	-2.1286945
CGGAGGTTGAGGCTGCAGTGAG	973	0	1	1322.5	4.7339053	5.850657
TTGCATCTTCTGGTTGAGCCCC	974	0	1	3115.5	4.8583755	5.3206172
GAGAGAGCTCTGTGCCTGGGAT	975	0	1	1460	4.1398292	2.7307003
GGCCCGGTGACGTCACT	976	0	1	2095	4.7288775	-1.6421453
TCTAGCTCTGCTTATCATGGCT	977	0	1	4019.5	11.909512	1.1704206
CTGGCTGGAGTGCAGGTGAGTG	978	0	2	4570	6.2398477	8.3825598
GATGGCCTCATGGCTGCAGGCC	979	0	1	902	4.7118134	1.0811797
GAGGCCAAGGTGGGCAGATCAC	980	0	2	2720.5	8.2338047	10.671504
GTCCTTCCACATGGCCAACCTC	981	0	1	3716	4.1157985	8.4863319
CAGGAGTTTTAAATCTAGCATG	982	0	1	1165.5	10.034127	-3.4165139
GGAGGGGCTCAGTCTTTCTTGG	983	0	2	2551	7.60566	8.0373402
AAGGCAAGGCTTCCAGCTCCCC	984	0	2	2465.5	6.0202217	6.2276101
TACTGCAACCTCCACCACGTG	985	1	0			
CACCGAGGCTGGAGTGCAGTGG	986	0	2	3565	11.145717	13.107421
CCACAGTCCTGGCTTCTGTCTG	987	0	1	4568	4.546155	15.062599
GCCCGCTGGCTGGGCTCCAGCT	988	0	1	3048	4.0028958	-8.7108431
ACTGCACTTCAGCCTGGGTGAC	989	0	2	21975	15.030581	28.149118
CTTCCCACCAAAGCCCTTGTTG	990	0	2	3477.5	6.069356	7.7381773
AAGTGCTGGGATTATAGGCATG	991	0	1	1598	4.0027814	6.5471692
TCGTGATCTGTCCACCTCGGCC	992	0	2	5621.5	23.653496	15.646881
GCGGCAGGAGTAAAGGAGGAAG	993	0	2	3316.5	10.005136	13.926331
GGCTCACTGCAAGCTCCGCCTC	994	0	2	20587	20.311087	3.6339736
GTGCCCAGCAGCAGCGTCCCCG	995	0	1	2773	6.90412	-1.4229031
ACTGTACTCCAGCTCTGGGTGA	996	0	2	8927.5	10.2185	21.731802
GGAGGCGGAAGTTGCAGTGAGC	997	0	2	2314	8.7133474	5.029707
TGGTTGTTAGGGAAGATTCATC	998	0	1	1996	5.7277908	-0.53821027

ACCTCCTGGCGGGCATCCTC	999	0	1	3524	4.3451629	9.1596689
TAGCTGAATTGTGGGAGACCTA	1000	0	1	1518.5	7.60566	-4.9874139
TCCTGCCGTCCTCCGGGGCCTC	1001	0	2	9326	11.404112	5.8492618
TGGTTGTGCACGGGTTGGT	1002	0	1	4287	5.809895	12.026738
TGTCCAGGCTGGAGTGCAGTGG	1003	0	2	9691	12.871147	16.345312
AAAGATGTTGCTGCTCCGCCCT	1004	0	1	10873	11.395624	-1.3708899
TGGGAGGCCGAGGCAGGTGGAT	1005	0	2	1509	6.3071833	8.9423923
TCACTGCAACCTCCACCTTCCG	1006	1	0			
CTCCTGAATTGTCCCTCACAGC	1007	0	1	3894	4.6719613	-2.2086017
CAAAGTGCTGGGATTACAGGTG	1008	0	1	2224	4.9705548	11.770996
CATGGTGAAACCCCGTCTC	1009	0	2	3678	7.6599259	10.599221
CATCCAGGCTGGAGTACAGTGG	1010	0	1	1197.5	5.0059147	6.9278154
TTGGCCATCTAAGCCCAGCCAC	1011	0	2	2464	9.1909533	7.750977
GGCCGCCGCCCTTGTGCTCTGC	1012	0	1	5552	9.3362026	-7.5507455
CCCTCTGGCCCTGTGGTGGAT	1013	0	2	65518	14.648276	19.804953
TAACAGATGTCATTTTCGGCGGC	1014	0	1	43807	16.818501	0.21859378
TCTCTTTCCTGCTGCCATCCA	1015	0	2	11985	23.580763	9.5384855
GCTCTAGTAGGAATGTCCCTCT	1016	0	2	6301	15.744108	2.9028673
AGCTCAATGCAACCTCCGCCTC	1017	0	2	11240	13.15651	6.5624309
CCTGGTTCAAGTGATGCCCCT	1018	0	2	11617.5	9.2222452	3.8587017
CACCTGTACAGGGCCGGGCTGG	1019	0	2	15471	7.5139775	10.770471
CTGCAGCCTCCACTTTCTGGGC	1020	0	1	2839	4.7054248	13.918253
GCCCCCGAGGAGGTGATGTCGC	1021	0	1	5201	12.058164	-2.6986685
GAGGTTGGGGCTGCAGTGAGCT	1022	0	2	2391.5	7.2082191	11.666763
ACTGCACTCCAGCCTGGGCGGC	1023	0	2	65518	25.924618	35.366241
CTCTGTGGTGGAGTGGGTCACC	1024	0	1	2634	4.6613207	1.0710925
GACCTTGTGATCCGCCCACTTT	1025	0	2	3834	7.5950313	9.0545225
GGGGCTTCTAGGGTGCCAGATC	1026	0	2	3012.5	13.356146	7.901947
TTGCTGACCTTTGCTCTCCGTT	1027	0	1	4311	5.1390486	6.5618801
AAGTGCTGGGATTACAGGTGTG	1028	0	2	3352.5	6.344357	13.838893
CAGCAGAGAAATTACATATTTG	1029	0	1	1053.5	5.0869894	0.55714673
TGGCTTTCTCACAGACCACCTC	1030	0	1	8109.5	13.15651	-1.1421698
AATAAACAAAGGACAAGGAGGT	1031	0	1	913	5.4493914	-0.35933188
GCTCACAGCCTCCCCCGGCCTG	1032	0	2	13198	7.8765292	3.4258959
GTGGTTCACCTGAGGTCAGGAG	1033	0	2	2687	7.6964669	6.9500546
CCCAAAAGTTCTGAGATGGCT	1034	0	1	1275.5	7.5570545	-0.66594625
CTGGAGGAGCTGCCATG	1035	0	2	3669	12.842446	14.933422
TGTCTATTCCTCCACCTCCGTT	1036	0	1	2379.5	4.5837574	3.2563431
GGCCTGGCAGAGCGCGCGGCTG	1037	0	1	3187	4.2506533	0.47298598
CCAGGCTGGAGTGCAATGGCGT	1038	0	2	1892	6.8911996	11.028392
CGCCCAGGCTGGAGTGCAGTGG	1039	0	2	12926	16.758549	16.607355
TGGCTCCTCACGTCCTCAGAGC	1040	0	1	1612	5.3898416	4.4133153
TCCTCCAGTTCTTGTTTCAG	1041	0	1	4451.5	4.743588	5.2467165
TGGTGGAATTGTAAAATAGTGT	1042	0	2	3325	12.173241	2.7421064
CGACCTTGTGATCCTCCCGCCT	1043	0	2	4594	6.1166434	4.4487605
TAGCTCCTCCAGATCTCATCT	1044	0	2	3659	10.385338	3.9473054
CCACGCATCCCTCCACAGAGAG	1045	0	1	2981	4.6559062	10.40073
ACCCAGGCTGGAGTGCAGTGGG	1046	0	2	4950	12.992976	17.386417
GCACCGCCTTGGACCGCCCGCT	1047	0	1	3964	4.1457386	10.605991
CAACATGGTAAAACCCCGTCTC	1048	0	1	2540	4.2821875	2.931881

GGCTGGGCCTCTCCCTCAGCTG	1049	0	1	6453	5.1583419	16.296978
TTTTCTCTTCCCTCTGGACCTG	1050	0	1	3826	4.9174376	7.1403542
AGGCCCCCTCCACCCATTCTGG	1051	0	2	2151	8.4221792	7.0899777
AGTTTGTGTAAGAAAAGC	1052	1	0			
TCAGGGCTGCACTGGCTGGTCT	1053	0	2	9852	10.620815	11.96568
CCCTCGTGCATCCATCATTTAG	1054	0	2	2096	6.675056	2.2716882
CACTGCACTCCAGCCTGGCCTG	1055	0	2	65518	20.659618	21.962681
TTCAGTCTCTAGCCCTAATTT	1056	0	2	5739	15.599205	7.8376389
AAGACACCAGAGACTGGCCTCA	1057	0	1	6306	5.8909965	5.1631103
CAGAGCTGGTGTGTCCTGGCAT	1058	0	1	4347	4.3130379	0.72330654
TATTGGCCGGGCGCGGTGGCTC	1059	0	1	3005	5.9769301	7.7475381
AGGTCTCTTGCTGTCTCTGGGC	1060	0	1	8026.5	6.4136252	0.43719938
TAGCCCAGGCTGGAGTGCAGGG	1061	0	2	6013	9.3222113	19.078527
CACTGCACTTCAGCCTGGGTGA	1062	0	2	65518	19.494125	35.251587
AGTGTTGGCTCGGCTGGCTGCC	1063	0	2	9220.5	15.521686	7.1320724
CTCTGCTGTGCCGCCAGGGCCT	1064	0	1	5084	6.4544711	0.20225658
TGCAATCCAGCCTGGGCGACA	1065	0	1	4499	4.9212852	16.91279
AGTGATCCACCCGCCTCAACCT	1066	0	2	5364	8.4659891	7.8198662
TGCCGTGGGGCTGAGGCTGGAG	1067	0	1	4521	4.5795527	15.352057
TTTAGATTGTGACCTCCCCCA	1068	0	2	5251.5	9.5200853	6.4590821
GGAGGCTGGCCTTCAGACGGGT	1069	0	2	65518	12.034198	25.266558
CCTGCCAGAGCAGCTTGTCCTC	1070	0	2	3950	6.2292013	6.3928571
TGGCCTCGGCATCCAGCAAGAG	1071	0	1	4673	4.4677706	4.3334913
CCACGGGCAGATGTGGTTGTT	1072	0	2	2023.5	6.754149	4.0614367
ACTGTACTCCAGCCTGGGGGAC	1073	0	1	3910	5.224843	16.213413
CCCTCTTGCTTCTATCCCACC	1074	0	2	7596	7.1978688	6.3785648
GCCACAGGCCCTGCTCTGC	1075	0	1	3930	4.9654756	0.13763157
GGCTGCTGGTTTCTTGTTTTAG	1076	0	2	7926	12.94939	11.212504
GGAGCCTCTGGCAGGGGGCCA	1077	0	1	2402	4.6396155	6.1019282
TCCTGGCCATCCAGCCTGGGGA	1078	0	2	16778	7.2028656	18.973217
TCTTGCCACTTCATCCCCTTTC	1079	0	2	5428	8.6937799	2.063446
GCGTCTCATCCTCCCGCTAATT	1080	0	1	2019	4.072968	2.8117723
CCTTCCCACATTCTTACATGC	1081	0	1	4637	9.2534456	1.1731225
CGCGCTCTCCTTCTGGCACCCA	1082	0	2	8509	6.424386	19.448072
GAGGCGGGCAGATCACCTGAGG	1083	0	2	1864	6.033988	5.7446184
GGGAGTTGTGGTTGGCTTCTGG	1084	0	2	4978	8.3206406	9.2158394
TGGGGCCATCTCACCCACTGTT	1085	0	2	1828	9.8785877	4.2386732
GCTAGGCTGCTGGCCACTGAGG	1086	0	2	6972.5	13.127683	19.686853
TGCCGCCCCGGCCATCTCGGCTC	1087	0	2	6915.5	13.391404	5.9536037
AGCTGGAATTACAGGAGCCCAT	1088	0	1	1223	9.1280918	-4.934659
GGGAACAGCTTGGGCTCTGCCA	1089	0	1	4814	4.5313773	3.7230809
CCCTGGCTCACTTCTGTTGTG	1090	0	2	20839	12.591182	5.4283981
TCACTGCAAGCTCCGCCTCCCG	1091	0	2	19903	18.896269	11.699102
CTGGACTGAGCTCCTTGAGGCC	1092	1	0			
CTGGGTTGGGGTTACATGACTG	1093	0	2	6057.5	6.2405562	7.4004421
CTGGTGTTGGGTCTTGCTTTTA	1094	0	2	4756	6.5764294	8.8639517
ACAGGCGATCCACCCGCCTCAG	1095	0	1	2228	5.9650521	8.9491081
TCAGGCACCTTCCTCTTATCTG	1096	0	1	2858	4.891077	9.5462265
CGGGTTCACGCCATTCTCCTGCC	1097	0	2	25616.5	15.660168	6.7002292
AAAGTGCTTCTCTTTGGTGGGT	1098	0	2	65518	11.238881	30.157898

GGCTCCCTGCAACCTCCGCCTC	1099	0	2	39003	18.926107	13.134951
AGTTGTTCTGTGGTGGATTCGCT	1100	0	1	3494	4.0696526	11.844742
GCTCACTGCAACCTCTGCCTCC	1101	0	2	52175	22.994247	20.293594
CTCCTCCACCCGCTGGGGCCCA	1102	0	1	4352	4.8429317	-0.27487165
TTATTGCACTCCAGCCTGGGTA	1103	0	2	45303	21.338472	22.149384
ACTGTACTCCAGCCTGGGAGAC	1104	0	2	8375	6.4653163	21.671926
ACAACCTCCTTCTTGGGTCCTGG	1105	0	1	6494	5.7869687	2.3521452
CCAGGAGTTGGAGGCTGCAGTG	1106	0	2	4602	7.9332623	12.632589
AAGTCTCTCACATATCTGGTCC	1107	0	1	3668	4.6719613	6.1481905
GAATTTTATTACTAGTCAACTG	1108	0	2	1889	7.8809133	3.6355321
GGCTGCTGGTCTTTCATAGTGGG	1109	0	2	12604.5	21.291653	18.561375
CACTGCAATCTCCATCTCCTGG	1110	0	2	5091	10.483025	11.471234
CCGGAGTGTCTGGCCTGCTGGG	1111	0	1	3411	4.093287	9.0740547
TCCCCTGGTGCCACGATCTGCT	1112	0	1	5256	5.5488677	-7.7961345
TCTTGGGCAGCTTGCTCGCCCC	1113	0	1	1661	5.9425497	-1.1524448
TTTCTTGGGGCCGTGTGCTGGT	1114	0	2	7386	8.0159159	10.662634
GGCTCTGCTTGAGGCCAGCCTG	1115	0	2	1496	8.5616169	2.8241165
TGGGTCCTGGCTGAAGATCTCT	1116	0	2	13345	7.4858232	22.909485
GCGGGCGGCTTCATCTTGCCCT	1117	0	1	5038	5.1213508	7.6892729
GCAGCTATTGTCTCCTGGGCCC	1118	0	1	3900	4.0808616	12.07268
GCCTTCCCACCACCCGTCC	1119	0	2	6139	7.5813851	3.1351645
GACCTCGTGATCCGCCCGCTTT	1120	0	2	4513	8.2720776	14.007803
CACTGCACTCCAGCTGGGTGAC	1121	0	2	7458.5	7.5623012	16.072519
CGTCCCGGGTTACAGCCATTCT	1122	0	2	4935	8.0834999	8.5963545
CTCTGGAGTGTCTGGCCAGGGT	1123	0	1	3361.5	4.2338123	13.302693
GCCTGTATTCCCAGCACTTTGG	1124	0	1	3873	6.2997189	-0.46441609
GGCGGTCTCAGCACCCCTCTTGG	1125	0	1	2606	4.5257893	0.3523702
TGCCCAGGCTGGAGTACAGTGG	1126	0	2	8395.5	13.998208	16.034225
ATCAGAGTAGTTGTTGCCAGA	1127	0	1	1471	5.5012255	7.6935115
CAGCAGCACACTGTGGTTTGTA	1128	0	2	65518	16.623587	30.172779
GCCTGGCCTCCTACAGTACTTT	1129	0	2	35866	15.014146	23.263319
ACTGCACTTCAGCCTGGGTGTC	1130	0	2	30071	14.363188	30.014778
GACCTCGTGATCCGCCCTCCTT	1131	0	2	6551	25.696636	10.76053
CAGTTTGTCCCCATGGCCATGT	1132	0	2	6591.5	13.401958	5.2375259
GGGCAGAGCCAGCCAGTCCC	1133	0	2	3180	11.937795	10.093319
GCTCATGACTGTAATCCCAGCA	1134	0	1	2783.5	6.7136006	1.7869294
GCTGCTCTCCAAGCCTCCTTGA	1135	0	1	3797.5	5.4047599	5.8530407
ACTGCACTCCAACCTGGGCAAT	1136	0	2	21062	16.688629	27.100132
GGCGTGCCCTGGCCCCGAGGCT	1137	0	2	28813	10.987214	21.873014
AAATGCAACGGGCTTTCCTTAT	1138	0	1	3531	4.3887382	1.0790982
CCCTGGAGGTTGAGGCTGCAGT	1139	0	1	1366	4.2553997	5.5404139
GCCCAGGAGGAGAGGCTGCAGT	1140	0	1	1922	4.5738077	5.7069306
TCAAGTGATTCTCCTGCC	1141	0	2	9836	15.970009	19.168186
GCCCTGTGCAGGTGTGCAGCAG	1142	0	1	1165	6.2430058	-0.72478187
CTTGCTGCCAGCCACCATACTG	1143	0	2	1793	6.5887036	2.1328712
TCTGCCTCCAGGAGCTGGCA	1144	0	2	12022.5	6.4897313	19.629604
TGATTTCAAGCCAGGGGGCGTT	1145	0	1	3186	4.1073384	9.1334038
TGGGGGAGCTCAGTCCAGCCCA	1146	0	2	3738	7.3541789	13.35856
AGGCCAGCCTGCCCAAAGCTGC	1147	0	1	1444	6.8652005	1.3340253
TTGTCCGTGGTGAGTTTCGATT	1148	0	1	2678	5.3224468	5.8358331

ATGGCCGCCTGTCCTTCCCGCC	1149	0	2	5678.5	6.8652005	8.8366051
CATTCTAGGCCTGGCTTGGGCC	1150	0	1	4350	4.3145142	0
CAGTGCCCGCCGCCGTTCTCTGG	1151	0	1	4235	4.8511839	14.764318
AGGTGCTGGGGCTTGGCCTGCT	1152	0	2	54992	14.781937	19.839622
CAGCAGCTCAGCCTCCTTCCCA	1153	0	2	6588	11.002058	9.0820408
CTCATTGTAGCCTCCAGTTCTTG	1154	0	2	5375	10.634505	9.6296253
CTCAGTGCTGCTGGCTCCTGTC	1155	0	2	30057	40.88406	25.543219
AGCCTGGGCAACAGAGCAAAAC	1156	0	1	2910	4.664422	-2.435894
ATTTACATACCCAGCAGCCTCC	1157	0	2	9344	14.651403	5.7202735
AAAGTGCTGGGATTACAGGCGT	1158	0	1	2149	5.1885619	11.850306
GCTCCACCTTAACCTTCACAT	1159	0	1	2577	8.7701244	1.6405232
CTACTGGCCATCTGATCTACAA	1160	0	2	4485	7.3851671	14.238548
TGCCTAGTTCTGTATTTACAGT	1161	0	2	1442	7.7322025	7.1628423
TACCCAGTGCCACCCTCTGAGG	1162	0	1	2340.5	4.2727714	6.8743863
AGCCCAGGAGTTTGAGGCTGTG	1163	0	1	2967	4.5458264	13.880125
CACTGCAAGCTCTGCCACCTGG	1164	0	2	4423	9.3773403	10.346853
CGCCTCCTCTCTGTCCTGATTT	1165	0	2	11564	15.306285	4.1242805
TAGCCCTGCCTTTGAACCTGG	1166	0	1	3340	5.771091	7.2742958
CACTGCACTTCAGCCTGGGCGA	1167	0	2	65518	19.854979	32.441864
CCCAGGAGGTGGAGGCTGCAGT	1168	0	2	1868	6.0943484	7.1866341
TGAGTGACCAGAAGTCCCCCTC	1169	0	1	2715	5.5675011	1.1538888
TTGATCTTTTCTTGCTGCCCCA	1170	0	2	12258	18.854212	2.8578236
CATTAGGACGCCCCGCCCATAC	1171	0	1	3517	4.7521834	7.6331592
GGTGGTTCACGCCTATAATCCC	1172	0	1	2909.5	4.9835281	4.240087
GTAGCTCTGTTTAAAGTTCTTT	1173	0	2	1147	7.4468746	3.0822921
AGGCGCCTGCGGGATCCTTGCC	1174	0	2	4344	8.3828068	9.3085003
GCACTTTGCCCTCCTTTGGCA	1175	0	1	3096	5.8571658	1.1003072
TCGCTCAGGCAGGAGTGCAGTG	1176	0	1	1902	5.7879028	8.7315207
TGCCAGCTGCTTGTCCCCCACA	1177	0	1	2506	8.8620977	-2.5429773
AAGTGATACGCCTGCCTCGGCC	1178	0	2	16691	9.2873106	2.0918362
GGGCTCTCCCACAACGTGCCAG	1179	0	1	2349.5	4.1230264	5.3486781
ACTGCACTCCAGCCTGGGTGAT	1180	0	2	65518	27.70583	35.281982
TCATCAGGGATATTGGCCTGAA	1181	0	2	2532.5	6.9170618	10.842815
GGGAGGCAGTGCTGGAGGCTGG	1182	0	2	9212.5	9.3155737	13.897033
CCAGTTCAGTGCTCACATCCA	1183	0	1	2332.5	4.5615263	1.8066665
TGCCTAGGTCTGGCCTCCTTGG	1184	0	2	10161	16.315468	2.7759731
CGGGGCCCTGGGGCTGAAGGTC	1185	0	1	4941	5.1423211	2.6783533
ATTGGTAGTTTTGTATTTCTCT	1186	0	2	2205.5	8.1146107	5.780735
CTGGCAAGAAATATATATCTTA	1187	0	1	1119	5.1329703	0.56972069
GCCGACTGCCTTGTGAGCCT	1188	0	1	3002	4.0046587	4.5328951
GCTCCAGTGACCATCGTTTTAG	1189	0	1	719	4.2234468	3.1870663
CCCAGGAGGTTGAGGCTGCAGT	1190	0	2	2825	8.4417934	12.283764
CGCCCAGGCTGGAGTGCAGTGA	1191	0	2	9513	14.644378	17.344313
CTCCCGGCTGCTCCGGCTCCCG	1192	0	1	3404.5	4.0221744	10.150807
GTTACTCCTGGTTGAGCTTGGT	1193	0	1	4309.5	4.4103327	15.300289
GCCTCCAGCCCACGCAGGCCTG	1194	0	1	4519.5	9.7356396	-2.5970438
TATTCATTGCCCATGTTTGTGA	1195	1	0			
CACCCAGGTTGGAGTGCAGTGG	1196	0	2	5832	13.915822	17.475407
AGAAGGGCTGGCAGGAGTT	1197	0	2	26652	14.563484	25.132761
GAAGTTTGAAGCCTGTTGTTCA	1198	1	0			

GCTTTATCCGCTTGACCCTTAC	1199	0	1	3616	4.4118524	13.271925
TCGCCCAGCTCATCTCCCACAA	1200	0	1	2703.5	5.3652906	1.3689227
GAGGCGGAGGTTGCAGTGAGCT	1201	0	2	4226	9.1032648	13.02844
GCTTGGCCCATTTGATCAGCTGG	1202	0	1	5906.5	8.7156487	-2.7078445
GCCCTGGGCAAGGTTCTGGCCA	1203	0	1	2714	4.0351701	-0.23995513
CTGGGAGGCGGAGCTTGACAGTG	1204	0	1	2035.5	5.6867909	7.8000135
AAAGCCTCCCAGGTTATGAGTA	1205	0	1	2572	5.2848206	7.2430992
GCACTGCTGCCTCCTGG	1206	0	1	2627	5.5307322	7.414557
GACCTTGTGATCCACCTGCCTT	1207	0	2	9694.5	12.58271	17.013798
CCCGGGAGGCAGAGGTTGCAGT	1208	0	1	1794	5.9571199	9.9902372
TGGCCTTGGCCGTGCTGGGGTC	1209	0	1	5712	4.9820457	-0.35016832
GAGGCCTGGGCAAGGGGGTCTG	1210	0	1	3266	5.8565254	9.1992407
CCAGAAAAATCCTCCCTTGTCC	1211	0	1	3211.5	5.2451043	8.3984203
GCTCCCACTGCTGTCTGCCAT	1212	0	1	9433	17.716768	1.6475885
GGCCGGGTGCTCTGGAGGTGCT	1213	0	2	14393	11.734104	12.172738
GGCTGGTTAGATTTGTGGTCTT	1214	0	2	21258	33.569485	15.757149
CTGAGGCAGGAGAGTTGCTTGA	1215	0	1	1306.5	5.4962068	-1.4525892
TCCCGTCTTGCTGTTGTCTGCG	1216	0	2	9875	9.1909533	2.2802107
GGTGTGAGACTTTGCATATCCT	1217	0	2	1808	6.4814534	9.6383839
CTCACTGCAAGCTCTGCCTCCC	1218	0	2	26494.5	19.073179	16.964733
CTGCTCTGCTGATCAGTGTCTC	1219	0	1	4736	4.4964242	11.948936
GGAATGGTGGTTGTATGGTTG	1220	1	0			
TGATATGTCCCTCGACATCAGG	1221	0	1	1273.5	4.8226123	7.3988724
TTGTCTTTTGTGGGAAATATGG	1222	0	1	1686	8.4781733	1.0731497
CACCATGCCTGGCTAATTTTTT	1223	0	1	4149	5.579587	14.67128
CCGAGGCTGGAGTGCAGTGGCG	1224	0	1	1129	4.6293564	7.4294724
CAGGAGCTCAGATGACATCTCA	1225	0	1	1856	4.9010544	10.314
GACCTCGTGATCTGCCAGCCTT	1226	0	2	4406.5	24.777288	14.546185
CTCTCCTTGGCCACCTCCATGA	1227	0	2	23276	9.521204	7.0737572
CCTGGCCGCTGTGCCCCCT	1228	0	2	40002	11.873036	10.703612
AGGTGCTCTGTGTATGCATAGA	1229	0	2	11593	19.340197	19.182079
AGTCGGAAGCTGTGCGTAAATC	1230	0	1	1043	4.256711	6.0202398
TGTCTGATCATGAGGCAGGGCT	1231	0	1	4775.5	4.5141959	-2.3209548
GCCCGCGGCCCGGGGTG	1232	0	2	9597	6.2839761	20.307545
CTCACTGCAAGCTCCGCCTCCC	1233	0	2	25071	20.895596	18.134468
CTTGGAGTAGGTCATTGGGTGG	1234	0	2	51071	16.39068	33.942337
TCAGCCAGCCAGCTACAGGCTT	1235	0	1	1054	5.2848206	1.757583
CATTCTGTGAGCTGCTGGCTTT	1236	0	2	6884	11.220102	9.6062307
TGCCTCCCTGGCAAGTCTCTCC	1237	0	1	4529	4.4007978	9.8346052
CAGCCCGCCCTGAACTTTCGGG	1238	0	1	2994	5.1533017	10.540549
CTTCCTCCTCCATCTCGAAGGC	1239	0	1	2834	4.6479778	8.16576
CTGTGCTCCCTCTGGCGCCCCG	1240	0	2	7554.5	6.8389502	13.825434
ACATGATTGTCTGGCTTGGCCA	1241	0	1	4115	4.3157549	-0.68419188
ACTATAGATGCTGGCGAGGCTG	1242	0	2	1628	7.8868184	9.2165308
TGGCTCATTCTAAACCCAGCT	1243	0	1	3232	5.0716186	3.3175437
GTGCTTAAAGAATGGCTGTCCG	1244	0	2	3362	12.66304	13.195816
GGACAGCCGAGTGGCCTTCTCC	1245	0	1	2573	4.0717006	6.836751
GGAGTGCAATGGCGTGATCTCA	1246	0	1	1123	4.2392659	5.4389768
CCCTGCATCCAAAGGCCTCCTC	1247	0	1	4119.5	8.5837584	-4.0344296
CTCAGGTGATCCACCCCTCTTG	1248	0	2	8190	8.7424583	3.9819176

ACTGCAACCTCCGCCTGCCAGG	1249	0	2	24273	17.594145	15.796898
GCTGCACTTCAGCCTGGGTGTC	1250	0	2	5310	7.5533419	15.940791
GCAGGTGGATCACCTGAGGTCA	1251	0	2	1573.5	6.542747	9.5370836
GGCCCTGGCAGCCACGAAAGCC	1252	0	1	2349	4.256711	8.8494081
TCAGTGA CTCTTCTTCCTGCT	1253	0	1	2889	5.3898416	-3.7892516
CGAGGCCTCCTCGCCGCCACCG	1254	0	1	2917	4.3228712	-0.75868702
TGGTGGCTCACACCTGTAATCC	1255	0	2	5307	8.9909515	17.038876
TGATCTCGTGATCTACCCGCCT	1256	0	1	1982	5.9927278	6.810081
GCTCACTGCAAGCTCCGCCTCC	1257	0	2	20232.5	20.168652	18.056574
CACTGCACTCCAGCCCGAGCAA	1258	1	0			
CAGTGACGGGCCAGTCCTGCC	1259	0	2	2112	9.479496	10.392011
ATCCTCCAGCTCCTGCTTCTGC	1260	0	1	3174	4.2183352	2.8458629
ATGCCACTGCACTTCAGCCTGG	1261	0	2	37857.5	13.168159	31.471567
CATTGCACTCCAGCCTAGGCAA	1262	0	2	35413	18.971554	24.194717
CGTTCAGCGGGCTGGCCGTGGA	1263	0	2	65518	10.117671	31.213285
AGCCCTCTTCCAGCCAGCACAG	1264	0	1	6035	10.519875	0.3822628
GTGTGTCTCCCAAGAAGGCCCA	1265	0	1	3536	4.6024246	8.0168934
TCCTTTCTCCCTCATCTT	1266	0	1	2966	4.4738102	11.3113
GGCCCAGGCTGGAGTGCAGTGG	1267	0	2	12915	16.751265	19.536619
TCGCACCATTGCACTCCAGCCA	1268	0	2	3636	8.0997972	12.774747
CCTCAAGTGCCTCCTGCTGCT	1269	0	2	5375	12.938377	9.593914
GGGAAATAATTAATGTGAAGTC	1270	1	0			
GAGGTGGGCGGATCACAAGGTC	1271	0	1	2041	5.9412212	9.3532887
TTGACATGCCTCCTACATGATC	1272	0	2	5065	12.953059	10.809283
ATTGCACTCCAGCCTGGGGGAC	1273	0	2	27662	16.315468	27.849897
CTCTGGACCCTCCTGCTGAGAG	1274	0	1	3192	5.8815751	12.393508
TTGGAATGCACACTGAGCCTGC	1275	0	1	1641	5.4196582	4.3278909
CCATGAATTCACTCCATGCTAG	1276	0	1	1780.5	5.4047599	0.20065525
TCCTTCACTCCCTCTGCATCCA	1277	0	1	3533.5	5.2938275	8.4558067
CCACTGAGGTAGCTGGTGA CTG	1278	0	2	2861	16.719574	7.8953633
TGTCTCTTTTCAAGCTACCCTT	1279	0	1	1480.5	8.1952085	-1.8686998
CGATGGTATCGGCCAGCCCCGG	1280	0	2	1767	8.5116291	3.1429348
CACCTTGTGATCCACCCGCCTT	1281	0	1	2139	5.5668392	4.7121377
CTGAGCTCAAGCGATCCTCCCA	1282	0	1	1617	4.0809031	1.5567338
AGGGTTGTGTGCTGGCCGCTGG	1283	0	2	65518	29.01285	32.102142
AGATTTCCCTTCCTGCTTGCCT	1284	0	2	5251	6.0291886	13.065763
ACACAGAGCCAAACCATATCAC	1285	0	1	1680	5.9849868	-1.285585
TCTCAACAGTGCAAGCTGCTCC	1286	0	1	4000	14.71687	-15.406388
TCTGGAGGGAAGCACTTTCTGT	1287	0	2	10399	6.8974981	22.211288
TGTCTCCTCGGCTGTCCAGCCA	1288	0	1	6736	5.2501798	5.3288264
CAGAGCCCCTCGTCTCCACCAC	1289	0	1	2694	5.538096	0.54361749
TGCTTGCTGTGGTTGGCTGGTA	1290	0	2	6974	21.75724	11.332961
TCCAGTCGGATAACTAGACGGT	1291	0	2	1198	8.0100813	7.3187399
ACTTGCTGGCTCCTTGCTTCTA	1292	0	2	8816	12.372648	16.758364
ACTGCACTCCAGCCTGGGCTAC	1293	1	0			
CTGAGCAGATGACCAGCCCCAG	1294	0	2	3552	7.8454118	5.6452436
GGTATATGGGCCTCACTTG	1295	0	1	716	4.1230264	3.7952623
GGCCGTGGTCGCTGACTCTCGT	1296	0	2	4980	6.9448657	12.094063
TCCTTCAGCCTCCCAGCTCAAA	1297	0	2	3775	7.1473608	4.387816
GCCTTGGTGGTTTTGGTAGT	1298	0	2	10696	15.110422	8.3110876

GTTC AAGACCAGCCTGGCCAAC	1299	0	2	16360	17.522753	9.7908163
GGAGGCTGAGGCAGGCGGATCA	1300	0	2	3046	8.4162111	8.6580906
GAGGAGCCCCCTCTGCC	1301	0	2	2540	6.3185239	6.9227304
GCAGCCATGTTCCCGTCTCAGCT	1302	0	2	2992	8.4334011	13.142536
CACTTCCCTTCTCTGCTCATGG	1303	0	2	7886.5	7.3931818	7.7415953
CTCTTCCTAGTGTGCAGCGTGG	1304	0	2	4232	15.394135	7.1230512
ACCAGCCTGGCCAACATGGCAA	1305	0	2	8606	8.2232008	18.60726
CCCTCTGCATACAGGCGAGGAG	1306	0	1	1363	5.7277908	-3.2187812
GTGAGGCGAAGGTGCTGGCGCC	1307	0	1	2222	5.5968246	2.6594312
ACTGGGGACTCTGGCCTTTTGA	1308	0	2	15830	9.3586321	14.166217
GATTACTGGTATTTGCTGGCTCC	1309	0	2	13394	25.892035	5.407784
AGCTGGTGCTCGGGGAGCTGGC	1310	0	2	65518	21.547987	16.272154
TCTCTATGCCATGCTGGCCT	1311	0	2	6926	17.665062	2.5852687
GCAGGGA ACTGGCTGGGCTTTTC	1312	0	1	9142.5	5.9037857	16.801399
TTTGGCTTCTCCTACCACCTCT	1313	0	1	4981	5.5610046	7.3423386
GACCTTGTGATCCGCCCGCCTT	1314	0	2	7757.5	11.425945	12.53443
AAACTGCTTCCTTGGCCT	1315	0	1	7436	5.6282043	5.6413546
TGCCTGCCGTAAATGTTACTT	1316	0	2	3936	12.749383	11.509386
TCAGGTGCCTTGGCTAATTGTT	1317	0	1	4158	4.3205009	12.139079
GGCGCTGGCCTGTGGGATCCCG	1318	0	2	65518	24.841112	31.449797
GGCTCACTACAACCTCCGCCTT	1319	0	2	14771.5	14.710124	15.748096
TCCACCAAGCCGGGGCCACTTC	1320	0	1	2648.5	4.7161036	4.8864894
CTCACTGCAAGCTCAGCCTCCC	1321	0	2	6344	15.211771	11.712019
CCCAGGTTGGCCTACAGA	1322	0	1	5095.5	4.6688876	17.382532
GACCCCTAAACCCGCTGGGCTG	1323	0	2	30088.5	13.552105	6.4749699
TGCACCACTGCATTCCAGCCTG	1324	0	2	41028	15.563788	31.684296
CCCGGGAGGCGGAGGTTGCAGT	1325	0	2	3131.5	7.7846441	13.396295
GCTGGCCACAGATCCCCAGGGA	1326	0	1	10408	25.43759	-5.445076
GGGAAGCTGGTCACCCACAGGC	1327	0	2	12450	11.913556	20.388573
AGGCAGAGAGGACCAGAGACT	1328	1	0			
AAAGTGCTTCCTTTTAGAGGCT	1329	0	2	7504	6.1279302	9.924984
AGCCCAGGCTGGAGTGCAGTGG	1330	0	2	12054.5	14.262013	20.370312
CTCCTCTTTAGCCCCAGCTGGA	1331	0	1	1799	4.2898717	8.4259157
GCAAAAAGTAGTGCTGGTTAGG	1332	0	2	9711	21.974758	16.433075
CAGGGATGGCGCTGGCTGCCCG	1333	0	1	7317	5.4272056	19.166769
CCTCCGGTCATTGTGCGGGCCT	1334	0	2	2835	7.0583911	5.132216
ACTCACTGCAACCTCCACCTCC	1335	1	0			
GGGGTGCGGGCCCCATCTGGCT	1336	0	1	49070	17.152702	-0.3207902
CAGCCCCACACGGTCTAGCTCT	1337	0	1	11400	8.6508255	-0.19845468
ATGCCACTTCATTCCAGCCTCG	1338	0	2	2970	6.3867145	3.6728451
AGATGGGGTTTCATCATGTTGG	1339	0	2	4401.5	10.491898	11.499362
GTGGTGTTTGAGCTGCCAGGGA	1340	0	1	2963	4.502933	8.8193016
GCGCTCTCTTCTCCTGGCCCGC	1341	0	2	65518	10.953011	12.865757
CACTGCAACCTCTGCCTCCCAGG	1342	0	2	34808	18.792194	12.987083
GCCTCCTGAGTAGCTGGGATTG	1343	0	2	7261	10.548355	12.900331
CTTTAATTGTAGCTCCATAAT	1344	0	1	3034.5	4.9478436	10.275362
AACCCAGGCTGGAGTGCAGTGG	1345	0	2	5616	13.703417	16.740423
TCAAGCAATTCTCCTGCCTCAG	1346	0	2	22552	20.397219	19.767324
ACAGTCCAGCCTAGTATGTATA	1347	0	1	1760	5.992043	1.5357794
TCAGGAGGCGGAGGTTGCAGTG	1348	0	2	2550	6.5481095	12.094613

AATGGTCTCTTTGTTCCCTGCT	1349	0	2	9183	7.6419687	3.2526188
GGCCGTCCCTAGAGATGGGGTT	1350	0	2	11689.5	8.4446125	7.2657032
ATCCTAGAATCAGCCCTTGCTG	1351	0	1	2772	6.7080827	-0.69137686
GGAAGCTCTGCCTAGATTTTCA	1352	0	2	7993	8.3658886	4.2364674
CTGGGAGGCAGAGGTTGTAGTG	1353	0	1	1370	4.1524282	5.7353191
GTCCCAAACCTCCTGACCTCAGG	1354	0	1	1638	4.5023069	7.1563048
TGGCGCGACGTGCCCCCTGCTT	1355	0	1	2537.5	5.5675011	1.0830367
GGCGTGGGCGAGGTGCTCTATC	1356	0	2	1796	7.1220169	4.9086099
CTCGGGCACCCCTGGTTCTGGTG	1357	0	2	65518	11.238881	23.126007
ATGGGCTGTCCATTGCTGGCTG	1358	0	1	4362	7.0200324	-1.9789392
TGAGCTTCCCTCCTGCACTACA	1359	0	1	2569	4.6559782	11.27425
CCCGGCACCTCCGCTGCACAC	1360	0	2	50589.5	16.062937	10.848449
GTGGGCATCACCAGGGCCTCCA	1361	0	1	1305	4.6559782	1.3485987
GAACCCTAGCATGTCCTTTAGG	1362	0	1	783.5	5.8142152	4.4672356
AGGGCAGGAGGTCCGTCCCTTC	1363	1	0			
AGGGCAGAGCGTTTCCTGCCCC	1364	0	1	1099	5.4493914	0.13351524
GCTTGGCTTTACTAGGGGGACA	1365	0	1	3943.5	4.974093	8.3365431
CATGAAATTGTATTGGCCTCAA	1366	0	1	1209	6.4949188	1.5365099
CACTGCACTCCAGCCTGGGCCA	1367	0	2	65518	31.247635	27.744917
ATCTGAGCTCCGCCTCCTGTCA	1368	0	2	3672	6.5016451	12.313261
TCTGCCTTTTACTAGCTGGATG	1369	0	2	12954	6.649405	9.6133747
ATGGGTTCAAGTGATTCTCCTG	1370	0	2	3260	9.7943249	13.811167
CATGTGTCTTGCTGCCCTCCAT	1371	0	2	11157	17.133692	10.310522
GCCTCCTGTCCCAGGCTGAGGA	1372	0	1	2413.5	5.771091	-1.0079587
AGGACCTGTAATCCCAGCACTT	1373	0	1	1119.5	4.0140038	5.6218853
TTCAAGTGTTTAAAGTTCTGCTT	1374	1	0			
CTGCCCCCAGCCTGGGCTTCGA	1375	0	1	1502	5.1329703	2.1353233
AGCTCCTGGCTTCAAGCAATCC	1376	0	2	14107	10.339123	18.669428
TGGCCCACCCGTTGA	1377	0	2	3982	17.579905	15.494586
AGTCCGTCCTGTCAAGCAGCTG	1378	0	2	19706	7.5470443	26.932724
CCGGGGTAGGCCCTGAGGCAGC	1379	0	1	4622.5	6.3919153	-2.5578749
ATGCCACTGCGCTCTAGCCTGG	1380	0	2	12177	8.2681303	19.851286
CATTATTCTCAGTTCTGTGCAG	1381	0	2	11732.5	27.869678	16.957344
CACCCGCTGGTCCCTGCAGTTC	1382	0	2	20816	8.5344362	27.261486
TACTGCACTCCAGCCTGGGTGA	1383	0	2	65518	22.371189	36.002476
GTGGCCCAGGCTGGAGTGCAGT	1384	0	2	14037	16.79743	18.340912
TCACTCAGGCTGGAGTGCAGTG	1385	0	2	2427	8.9816837	12.445157
TACCACCATTTGCCTGCTGTAT	1386	0	1	2224	5.3224468	6.6427116
GCCCTCCAGCCTGTGGAACCGG	1387	0	2	2293	7.0838871	2.9603255
CGCCCAGGCTGGAGTGCCAGTG	1388	0	2	4722	9.6376123	13.758563
ATGGTGCTGGTGGGAGTGTATT	1389	0	2	4053	18.971554	14.625937
CCAAAGTGCTGGGATTACAGGT	1390	0	1	2646	5.0643582	9.7789927
AGCGGCTGGCGGAGGACACG	1391	0	1	8764.5	5.8134389	21.684513
ATGCCACTGCACTCCAGCCTGG	1392	0	2	65518	26.690199	28.459244
CCTTTGATTTCCCCCGTCTCAG	1393	0	1	2348	4.8108587	4.7235146
GGGTTACTCTGTGTTGGTCAGG	1394	0	2	7310	8.6937799	12.815997
GCCCATAGTCTCTTTCTTTCTT	1395	0	1	1838	6.1946688	-2.755475
ATTGCACTCCAGCCTGAGCAAA	1396	0	2	46579	22.505102	33.557095
CACTGCACCCTCAAACCTCTGG	1397	0	1	6945.5	5.9455066	1.1890075
TCCCATGGGGCCAGCCGCCATC	1398	0	2	3581	15.749751	10.859034

CACTGCACTCCAGCCTGGGCGA	1399	0	2	65518	30.700432	26.58386
GGGGTCTTGGAACAGGTGGCCCT	1400	0	1	1856	5.8500195	-1.9162606E-2
CACTGCAGCCTCAAATTCCTGG	1401	0	1	4509	5.5284224	3.5514677
TGCAGGCTCTTGGTGACGTGGG	1402	0	2	2639.5	6.3321967	6.947082
GGTGGCCCCTGGGAGATGCTGG	1403	0	2	65518	31.295538	14.111359
AACCAAGCCAGCCAGCCTCTC	1404	0	2	4971	17.613102	15.532504
GCCCAGGCTGGAGTTCAGTGGT	1405	0	2	1573.5	6.542747	8.0195217
AGCCTGCGATCCCACCTGGCCT	1406	0	2	20991	9.0031242	4.5749111
TAACCTCTCTGTGCCTCAGTTT	1407	0	1	4997.5	5.1691394	10.657457
TAGCATGGCTCTATGGAACA	1408	0	2	1393	10.196934	8.9662762
CTGGCCTATCATAAGCATTTT	1409	0	1	65516	13.391268	1.4583727
CAGCCTGGTCCCCGGCTCACCC	1410	0	1	3234	4.2474666	6.4346752
GCCCAGGCTGGAGTGCAGTGGC	1411	0	2	24154	17.516109	26.539131
CCAGGCTGGAGTGCAATGGCAT	1412	0	2	2590.5	6.1812749	11.923506
CACTGCAATCTCTGCCTCCTGGG	1413	0	2	27656.5	19.716053	17.422838
TGCCTCAAGCCCTCCACTGCAC	1414	0	2	6112	10.263255	7.5186887
GACCCATCCTCCACTTGGCAGC	1415	0	2	2498	6.505065	6.8388047
AACCACCATTCTCTCCTCTTCC	1416	0	1	2979	4.7405486	1.3000224
TTCCATTTGGAGCTCGCAGCCT	1417	0	1	5965	4.9900851	14.792343
AAGGTTCTCTCTCCACCCAGC	1418	0	1	2925	4.0868788	6.821908
CTCCTGGGAAAGGCTGGACACA	1419	0	1	2176	4.3887382	5.3727546
ACTGCACTCCAGCCTGGGCACA	1420	0	2	65518	31.833015	34.428837
TCACCAGCTCTGCCTCGCCAGT	1421	0	2	10572	6.2146297	17.905064
GTTGCCTAGGCTGGAGTGCAGT	1422	0	2	3942	8.7036104	9.8695612
TGCCTGGCCTCTTCAGCACTTC	1423	0	2	27021	10.873885	26.68429
CCCTGCCAGCTCCCAGCA	1424	0	1	2367.5	5.8455133	7.8306561
GAGGCCTCAGCCTGCCCTGAAC	1425	0	1	1470.5	7.0200324	-0.58433282
TCACTGCAAGCTCAGCCTCCCG	1426	0	2	6757.5	12.953059	11.945885
TCCAGGCCCTCAATCCATTTCOA	1427	0	2	8934.5	13.815792	9.5553522
AAAAGCAATTGCGGGTTTTGCC	1428	0	2	4663	15.116411	4.7130346
TCCTCAGAATCACCTGGCAGCT	1429	0	2	2574	6.6020346	3.5169666
GGGTTCAGTCCCTCTTGCTACT	1430	0	1	3765.5	4.6101117	4.239377
TAGTTTCATCTCCACCCTGCCC	1431	0	1	2083	5.4642267	0.15956412
GGGTCTCTGTTGGCTTCTT	1432	0	2	11264.5	7.8554482	5.5741806
GGGGAACGCGCTGGCCCGCGCC	1433	0	2	7005	6.2445078	11.806351
AGGCGGAAGATGGCCCCATAGA	1434	0	2	1471.5	6.9170618	3.567507
TCTCTTCGCTGGCCCTCGGGGA	1435	0	2	47791.5	15.379544	20.008915
TGCCCAGGGTGGAGTGCAGTGG	1436	0	2	6671.5	10.579865	17.748798
AATTGCTTGAACCCAGGAAGTGGA	1437	1	0			
GCACACGGCAGCCTCCTCCTGA	1438	0	2	2910	8.0682802	10.311243
CTCCTGCTTCACGGGCACCGCC	1439	0	2	10401.5	13.127683	2.1750216
CCCTTTAGCCCCTGCAGAGACT	1440	0	1	39494	29.852627	0.54301858
TATTGAGACCAAGTGCTTGCTTA	1441	0	2	1212.5	10.770452	7.2894559
TCGCCAGGCTGGAAGTGCAGT	1442	0	2	2518	8.9316044	12.591391
GCTCTGCCAGCCCAAGGCGCAG	1443	0	1	5831.5	4.9416537	10.837112
GGAGGCGGAGGTTGCAGTGAGC	1444	0	2	3959.5	10.600774	13.769753
CCCTCACTCCTGCCGGG	1445	0	1	5527	5.4066739	-0.32305354
GCCCCTGCCTTTGAACCTGGAG	1446	0	2	9052	20.457079	3.550808
TTCTCCAGTGCGGTAGCCAT	1447	0	1	2372	15.630626	0.20187679
GCTCCTTTATTTTCTCTCGTGT	1448	0	1	2092	4.9322701	6.8224359

CATTCTCAGTATCAGCCAGCCC	1449	0	1	2579	12.640401	1.6748168
TAGCAGAAGTTGCAAACCTAGGG	1450	0	1	964.5	4.0301342	0.67141521
CCAAGCAGAGCAGCCTCTCTGG	1451	0	2	50138.5	17.876169	21.568254
CTAGGCTGGAGTGCAAGTGGCAC	1452	0	2	2019.5	7.9472141	11.208291
TTCCTGCGCCCTTCTCGCCCGC	1453	0	1	6532	6.8755865	-0.67481649
CTGTGCTGGGTCCTTCTTTTGA	1454	0	2	3805	10.533696	10.867439
AGCTCACCAACCTCCGCCTC	1455	0	2	18085	14.695093	9.1603575
AGTCTTCCCAGAGGAGGTGCCA	1456	0	1	1153.5	6.3185239	-1.0385203
GAGGCGGAGGTTGCAGTGAGCC	1457	0	2	2617	7.804688	11.36616
GCCCTCCTGAGCTAGCACGTGT	1458	0	1	12521	12.908952	-0.01282406
CATTGCACACCAGCCTGGGCAA	1459	0	2	65518	23.259714	27.904207
AGTTCTCTTGCTTCAGCCTCCC	1460	0	1	8418	8.3884401	1.3339518
TCCAGCTGTCCACGTCTTCCTG	1461	0	1	4070	5.0534353	4.2019873
TGCCTGGCCTCCTGATTCCCTC	1462	0	2	37634.5	13.004288	2.9085336
GCCTCCAGGGATGATTCCCTCC	1463	0	2	2862	10.98442	5.283977
GTCCCTGAGCCTGGCATTTCCTC	1464	0	2	9774	6.3336153	2.3762388
ACTGGCCAGCCAACAACAATAG	1465	0	1	877	5.0408092	-4.5819459
GCTGGCTCCACCTGCTGCCAGG	1466	0	2	2916	6.3332305	13.052609
GCCCCAGCCTCCCGAGTAGCTG	1467	0	1	2330	5.0814857	9.9303665
TCCCAGCTCCTGGGCCCCACAG	1468	0	1	5372.5	4.7662401	7.1915674
CACTGCACTCCAGCCCGGGCAA	1469	0	2	65046	15.988069	31.551188
TGACCTCATGATCCGCCACCTC	1470	0	2	11003	34.517956	15.899262
GGCCGCTCTCCGGTGTGGATCT	1471	0	2	13720	8.1071081	18.136568
CTAAATGCCCCCTTCTGGCACAG	1472	0	2	63453	11.163343	20.293009
TCACTGCAACCTCTGCCTGCCA	1473	0	2	25898	18.696442	17.538256
CCGGTGTTCAAAGTCTGGTATG	1474	0	2	6055	6.6824059	12.060349
CACCCAGGCTGGAATGCAGTGG	1475	0	2	3367	10.824119	13.172818
CACCCAGGCTGGAGTGCAGTGA	1476	0	2	2243	8.5379591	11.457872
TTCCATATCTGTTGCATATCAT	1477	0	1	1059	4.0724583	4.4120793
CCACTGCACTTCAGCCTGGGTG	1478	0	2	61492.5	17.94875	20.821732
GCCAAATAAGTGTCCGGCCCTC	1479	0	1	5930	10.101467	3.6227588E-2
GCCCGCGCCAGCCTCTCCATCT	1480	0	2	3281	7.5448685	10.447037
CATTGCACTCCAGCCTTGCGAA	1481	0	2	16173.5	8.520524	19.366573
TGATAGATCCATATTTTGGTAA	1482	1	0			
TGCTCGCCCCACATGCCCTCAT	1483	0	2	5021	8.3489428	2.7518404
TGCCTGCCCCAGCTGAGATATC	1484	0	2	5686	10.380668	15.221783
TCACTGCAACCTCTGCCTCTTG	1485	0	2	48652.5	22.205072	18.44136
TGGAGGAGAGTTTGTCAGTATAG	1486	1	0			
CCCAGGCTGGAGTGCAGTGGCG	1487	0	2	5921	13.471205	18.407236
CACCCAGGCTGGAGAGCAGTGG	1488	0	2	2370	8.847928	11.617569
TCTGCACCATCGTATGCTTAAT	1489	0	1	3861	4.0593572	6.2677927
CTCTGAGCTGCCTTTTGAGCTT	1490	0	1	1602.5	4.3898053	5.8146801
TCCCGCCCTTGTAATTGCCGAG	1491	0	1	5151.5	5.9488397	7.757297
CGCCCAGGCTGGAGAGCAGTGG	1492	0	1	1602.5	5.2608914	6.5835171
GGTGGCTATGGCTGTGCTCGC	1493	0	2	3426.5	15.917648	2.9563422
CCTAGAGCCGCACCTCCTCCAC	1494	0	1	2369	5.835712	4.0593348
GCCTCCCCAAGCAGCAGGGATT	1495	0	2	2657	6.1669488	6.5350518
AGAAAGTGCTTCCCTTTGGTGA	1496	0	1	4890.5	5.1180902	15.543441
ACCCTGGCCGACTGCCCTT	1497	0	2	35652	12.982363	11.41268
TGCTGCACCCTCTGCCTCCGGG	1498	0	2	6094.5	6.9428978	10.588869

CAGGAGGTTGAGGGTGCAGTGA	1499	0	1	1559	5.1060648	7.4941492
TGGGATGCTCAGGGCCTGGAGC	1500	0	1	1824	8.0682802	0.78988832
TGCTCTGATTTTTGCCCCAGC	1501	0	2	7060.5	10.413313	7.7476549
CGTCTGGCTTCTCCACGGTAAA	1502	0	1	8462	5.8395977	11.586881
TGTCATAGTGTGGTAGCAGTGG	1503	0	1	2076.5	12.082075	-3.4609232
TGTGGTAGTCACGGCCCGCCAC	1504	0	2	5909.5	23.027369	15.816967
CTCTGCCTGTCTCATCCTGCAA	1505	0	1	5028	4.6244407	0.84503251
CATCTTTGCCCATCCACTTCCA	1506	0	2	3944	14.688863	11.31537
GGCTGGTGGCTGGTTCTGGACC	1507	0	2	20736.5	31.680035	17.914019
AGTGGTCTTAGCTTGCTGGGCT	1508	0	1	2958	11.094181	1.2701284
CCCCTGCTGTGCTTGCATGGCT	1509	0	2	12605	18.076384	11.74684
AGCCAGCCAGCAGGTATGC	1510	0	2	2011	11.254579	11.186662
GAGGCTGAGGCAGGAGGATCAC	1511	0	2	13980	11.834332	23.254768
ATGAGCACACTGATAAGCCCCT	1512	0	1	3757	9.4285412	-1.0390751
AGTGCTATCGAGTTCTAATGCT	1513	0	1	1529	11.816049	-1.6991031
CAGCCTGTAGTCTGGTCCAGGT	1514	0	1	1863	5.1711364	10.847687
CTGGCTCCTGTTTAACCAGCTG	1515	0	2	2294	6.0272546	8.8361721
GTCCCCTGTCCAGGGCCAGCCA	1516	0	1	3915.5	9.6158686	-3.1074336
CTTGCCTGCCCTGTGTCATAAA	1517	0	2	5903.5	11.970026	3.0393276
TCCCGTAGGTTGCTGTAGTCGG	1518	0	1	3606	5.655231	9.4085045
GTTGGCCAGGCTGGTCTCAATC	1519	0	1	2090	5.0410533	-4.0856218
TCTCCCAGATCCTTTAGCCTCC	1520	0	2	7384.5	14.663905	2.166656
GCCTCCTGGGGTGCCATCATCT	1521	0	1	8207	11.668092	1.0917441
ATCATTAACAGTGCAGGGGTAGG	1522	0	2	1291	6.7080827	6.8988318
TGGCCACCACCAATACTTGCCT	1523	0	1	1777	4.5837574	0.96471441
GGCCTCCCGGACCGCAGCGCC	1524	0	1	1805	4.437829	2.6645198
AGCCCAGGTCCAGTTCACTGCA	1525	0	2	910.5	6.2636547	2.1727333
TCCCCTCTTGCTTGGTCCAGA	1526	0	2	10285	8.0190945	16.142628
CTGGCCTAGACAGACCCTGATC	1527	0	1	24673.5	24.969994	-5.0956011
CCCTGGCTGCGTGATGGATGAA	1528	0	1	3966	4.1167688	10.868774
GTAGGCCATGGTGGTTGTCTCT	1529	0	1	2289.5	4.7606225	9.7036562
TGTGGCTCAGGCGGCTTCTCCT	1530	0	1	7641	5.5752053	5.2592807
TCCCTGTGTCTGCGGGGCACCT	1531	0	1	3722	5.4018469	0.76068252
ACCTGAGCTCCACCTCCTGCC	1532	0	1	3490.5	5.5675011	2.1058514
CCCAGCGAGTTTGCCGGTGAAC	1533	0	1	1491.5	8.489337	0.20919423
TTCAAAGGGAAAAGCAGGCTGG	1534	0	1	7722	5.5424767	6.6963782
CGGCCCTCCTCTCGCGCC	1535	0	2	4246	7.6359258	11.74948
AAGTGATTACAGCCCTCA	1536	0	2	4389	9.3773403	14.014197
GGCCTGGGCTCCGGGAGTTACT	1537	0	1	3130.5	4.0424356	-4.2492251
CCTCGGCCGAGAGCCAAGTGC	1538	0	2	2066.5	16.716997	8.8393974
TCTGTGCCTGCTTCCCCACCCA	1539	0	2	4441	10.529091	6.8799772
CTGCACTCCCGCCTGGGC	1540	0	2	11228	7.6034174	5.8922038
GCACTCCAGCCTGGGTAACAGC	1541	0	2	65518	29.270939	27.328928
CTGGAGCAGACAAAAGG	1542	0	2	8594	11.848651	3.8546574
CTCACTGCAACCTCTGCCTCCC	1543	0	2	48422	21.955811	20.696438
TGTGCCTAGTTCTGTATTTACA	1544	0	2	2504.5	10.873516	8.0277433
GGTTTTACCTCCAGAATGTGC	1545	0	2	2724	8.9372482	2.5630777
CGTAAGTCACAGCGCCTGGCCC	1546	0	2	38826	11.506068	25.787857
CTCTGTGATATGGTTTGTAAATA	1547	0	2	6862	19.265455	13.692534
TCTCCCCTGGTCTCGCGCGCTG	1548	0	2	21744.5	8.1104021	2.3839858

CACTGCAACCTCCACCTCCTGG	1549	1	2	31393	19.150194	22.611071
CTGGTAGCTCCTGAATATCCCT	1550	0	2	2223	17.251909	5.7171526
ATGCCTGTAATCCCAGCACTTT	1551	0	2	8871	12.921462	20.372988
ACAAAGCGCTTCTCTTTAGAGT	1552	0	2	65518	11.238881	26.766436
AATCGCTTGAACCCAGGAAGTG	1553	1	0			
GGGCTTTTGAATGGTCTGT	1554	0	2	4463	9.6709318	2.0551727
AGCAACTCTCACCTGGCTGC	1555	0	1	7806.5	5.9086308	13.562915
TGCCCTCTTTCTGTACAGCTCC	1556	0	2	6133	10.524484	4.3130703
TGGTTTTAGGGAATCAATCTAT	1557	0	1	2404	5.3749018	0.52072495
TTCCCACTGTGGCAGAGCCTCG	1558	0	2	4853	8.5227718	8.7430191
CGTGTAGCATGCGCCACCACCA	1559	0	1	1152	4.372324	-1.7681072
TGCCTAGGCTGGAGTGTAGTGG	1560	0	1	1960	5.1336985	-5.655652
TACTCTTTTAGCCCCACAGAGA	1561	0	2	7108.5	14.535069	18.807434
CAAATCCCTGCTCTGTGCTG	1562	0	1	3854	4.0554743	15.468264
CCAAGGTGGGAGGATTGCTTGA	1563	0	2	65518	19.42584	35.754147
CCAGACTGCTTGCTTCCCAGCC	1564	0	1	14958	21.194012	-0.46141499
CTCTGCAAGTCCAGCCCCTGGC	1565	0	1	4339	4.6901293	-2.0411224
TGTGAGACTTTCTTTGGCCTCT	1566	0	1	2660	6.6352882	0.18635188
CTCTGAGTCCTGCACTCACCCG	1567	0	1	2770	6.7869315	1.284364
ACTGCACTTTAGCCTGGGC	1568	0	2	28568	11.638906	27.546202
TCAGCCATTTCCTTACCTTTC	1569	0	2	3289	10.019641	3.658488
TCACTGAAACCTCCACCTCTCG	1570	0	2	4339.5	9.3257465	9.4827623
AGATTTGGTGTCTGGTTGATAT	1571	0	1	3906	5.6260681	15.079812
CAGGCCTCTTACCCTCTCT	1572	0	1	2175	4.1754398	3.2060738
ACGCGCTGGGGCGCTGGCCAAT	1573	0	2	65518	13.337035	9.5484018
CCTGTGGCGGGGGCCAGTGCCCT	1574	0	2	2732.5	7.5204544	6.9828696
CACTCAGCTGAGCCCTCAGCCC	1575	0	2	3808	6.236114	7.0009232
TCCCCCACTGTTTCTGCTAC	1576	0	1	4143.5	4.8829288	1.3394566
GCCTGTCCTCTTCCGCCTGTCT	1577	0	1	14508	12.145576	1.6282115
CCACCTGAGATAAGAGAGCTCA	1578	0	1	1308	5.8285513	3.6287591
CCAGGAGGCGGAGGTTGCAGTG	1579	0	2	4649	9.3886547	16.137344
TCACTGCAAGCTCCTCCTCCTG	1580	0	2	12173.5	21.173698	8.2767439
GTATTGCTTGAGCCCAGGAGTT	1581	0	2	65518	20.541035	33.582275
CCCTGGCTGATACCGGAAAGGC	1582	0	2	9281	7.5079288	7.661869
CTCACTGCAACCTCTGCCCCCA	1583	0	2	39028	21.537285	22.098822
CACCACTTTCTCCTTCTCCTTGG	1584	0	1	3132	5.2580366	8.4857149
AGGAGGGGTTCTCGGGTGCTGA	1585	0	2	1395	7.4959846	3.0751243
GTAGACCATTATCTGGGGAGT	1586	0	2	3261	18.415466	9.8317289
TCTGCACCCCAGCCTGAGTGA	1587	0	1	3009.5	5.033093	10.499595
TGCCTAGGCTGGAGTGCAGTGA	1588	0	2	2695	6.3287864	5.4875331
CCTTTTATCCCCTAATTGGCCT	1589	0	2	8596	19.616385	9.8835402
AGAAAGTGCTTCCCTTTGACT	1590	0	2	11968	7.2289524	23.562014
TTGTCACTGCACTCCAGTCTGG	1591	0	2	12372.5	9.9857264	24.029345
TTGCTCTTGAAAATTGATGCTG	1592	0	1	18285	23.095486	0.6942786
AAGCCAATGCTAGCCCACATGC	1593	0	2	3477	8.0798817	10.92757
TCTAATCCTATGGTGGGGAGGG	1594	0	2	1947	8.5338745	6.3978777
CGTGCCACTGCACTCCAGTCTG	1595	0	2	29565	13.984879	26.717236
CCACTGCACTCCAGCCTTGGCA	1596	0	2	65518	19.59687	23.317396
GGCGGAGCTTGCAGTGAGCCGA	1597	0	1	1587	4.3907022	2.4575887
AGCTGGAGATGAGTGACGTGCC	1598	0	1	10661	16.698954	0.85748941

TTTTGGTTGTTGGGTAAGAGTA	1599	0	1	2392	4.963624	5.6073937
TTGCCGCCGTCTGCTCGCCCCG	1600	0	1	4152.5	4.4578457	2.1733229
TGATGTGGCCCCACTTAGCTGT	1601	0	1	2921.5	18.344973	-1.1306779
TGACCTCATGATCCGCCACCT	1602	0	2	7185	29.981552	13.353135
GCCGTCCACCTCGATGGCCACT	1603	0	1	4073	4.6692619	-8.5749388
GACAGGCTTCCACTATGTTGCC	1604	0	1	1321	5.3749018	6.195621
TACTGCACTCCAGCCTTGCCAA	1605	0	2	18364	10.029301	16.731598
CTCTGTAGAAAGAGCCCAGGTG	1606	0	2	1166	10.625381	5.0621781
TTCTTTTCTGAGCCTTG	1607	0	1	3674.5	4.927527	-1.7429894
GACGAGAGACTCCATCCACCAC	1608	0	2	1036	6.9557924	5.046813
ATCTCAGCTCTGCCTCCTGGGT	1609	0	2	8963	12.361974	12.799247
CTGGAGGTGCTTCGCTGGCCAC	1610	0	1	33822	24.215584	-8.2400523E-2
TTCCCTTAAATTATGGCATCTA	1611	0	1	4395	7.3068743	-0.26304191
TTAGGCCTTTGATTGGGGTGCT	1612	0	1	1685.5	4.1420093	7.9094262
CCCATTCTTGAGTTCAGCTCT	1613	0	2	3582	13.552105	2.9659367
GAGGGGAGCCCCCATCCTCCAG	1614	0	2	3509	6.0553408	8.2040138
TTCTCCCTGTCCTATCAAGACT	1615	0	1	4699	4.7479568	12.121504
TCATTCCCTCATTGTTCACTGG	1616	0	1	8088	8.6392965	1.1877192
GGGGGCTTGCCCCGGTCTGGTT	1617	0	2	17107.5	8.3545551	12.59028
ATGGGCCTCCTATTATCCCCAT	1618	0	2	4745.5	13.363207	5.1394033
GCCTGGATTCTTGTTTCTCAG	1619	0	1	2049	4.3417811	7.2988648
TGTGGGTGGCATCGTCCTGGCC	1620	0	1	9679.5	6.8719993	0.49652323
GCCGGGTTCAAGCCATTCTCCT	1621	0	2	3787	7.9569592	12.92104
GCCAGCCAGAAACGTCACACTG	1622	0	2	3409	16.32616	4.566371
CTCACTGAAACCTCCGCCTCCC	1623	0	2	18912	16.516399	5.5995822
GTGCTGGTGCTCGCTCCTCTGG	1624	0	2	8165	11.725875	9.7062302
TGCCCAGGCTGGAGTGCAGTGG	1625	0	2	22039	16.547016	22.788761
TAGAGTGTCATAACAGTGCCCA	1626	0	1	1991	9.5302086	1.9559761
TATGCCACTGCTCTCCATCCTA	1627	0	1	3874.5	5.9149723	1.1388568
TGGTCTGCTGAACAGCCGTATC	1628	0	1	1757	4.743588	1.0271198
ACCAGCCTGGCCAACATGGTGA	1629	0	2	14312.5	12.221603	21.144381
GCCAGCAGCTTCTTCTCATCCT	1630	0	1	12277	6.6476259	-3.0264895
TGGCTCTGTCCTCAGCT	1631	0	1	6081	5.0312958	9.2481689
ACCCAGGCTGGAGTGCAGTGGC	1632	0	2	6072	13.647521	18.928474
TCCCCAGCTTGCTACTTCTGCT	1633	0	1	3083	5.0408092	4.8841767
CTTCCCTCTGCTCCTTGGTCCA	1634	0	1	19594.5	9.4720697	1.9364738
CTTCTCGGGGTTCCCGCGCCCT	1635	0	1	2766.5	4.3488479	3.1100295
AGGGAAGGACTGCTGGGTTGGC	1636	0	2	10310	6.1609344	2.3204882
CCTGCCTATGAGACGTTTTGCC	1637	0	1	2184	7.8809133	-5.31426
TTTTCTTCATATCCCTTATGT	1638	0	1	1319.5	4.0893412	-2.6567316
CATTGCACTCCAGCTCTGGGCG	1639	0	2	59621	23.220642	28.257877
GGGAGGTTGAGGCTGCAGTGAG	1640	0	2	3383	10.8508	12.95626
GGCGGCCCAGGCGCTTGAGAT	1641	0	2	6899.5	8.1672001	10.434432
GTGCTGTGCCCTCTGCTGGGAA	1642	0	1	3638	12.00617	-1.0814483
AGCAGAGCAGTCTCCGCTCA	1643	0	2	11919	6.4712315	22.303505
TGGCACAGCCTCCATGTCGTCC	1644	0	2	2677	6.0342832	3.5939596
GCCTCAGTCTCCCAGTAGCTG	1645	0	2	11503	10.848304	18.821283
CGCGCCGTCGGGTCCAGCC	1646	0	1	2247.5	4.7277126	7.7918286
CCCCGAGGCTGGAGTGCAGTGG	1647	0	2	8152	11.888549	9.8740635
CGTGCTGGGTCTGCGGGGCCGT	1648	0	1	5352	9.8540783	-5.7792974

TAGGCCCTAGTGCCACGTGGC	1649	0	1	1019	4.9789224	-0.50027198
GACCTTGTGATCCACCCGCTTT	1650	0	2	4584	8.4290171	13.331941
CCCTGGCTGGCTCTGCCCGGAC	1651	0	1	5439.5	4.9906063	0.71976095
GCACTGGCCGCACGCGTAGGGC	1652	0	2	11799	10.682883	23.348194
GACCTTGTGATCCACCCGCCTT	1653	0	2	8371	11.550721	15.977306
CAAAGTGCTGGGATTACAGGCT	1654	0	1	2028	5.1953826	10.857911
TGGTGGCTCACGTCTGTAATCT	1655	0	1	1871	5.7638865	-7.8935137
CATCCAGGCTGAAGTGCAGTGG	1656	0	2	2134	8.2575912	10.422696
TGATATGGTTTGGCTGTGTT	1657	0	2	4515	12.488225	16.236593
TCCGGGAGGCAGAGGTTGCAGT	1658	0	1	1221	4.4037938	7.4545732
GGTGAATTTGCCTCCCGACTGA	1659	0	1	3632.5	5.797946	13.529587
GGGTGCTTTGGCTCACGCCTGT	1660	0	1	2429	4.6753616	12.409147
TTCACCATGTTGGCCAGGCTGG	1661	0	2	8459	14.352482	9.058075
TGGTGCTAGTTAAATCTTCAGG	1662	0	2	2715	17.999035	10.341267
CCTCGGCTGGGCCTTGGCCACT	1663	0	2	7735	6.1994433	14.162719
CTCACTGCAATCTCCGTCTCCC	1664	0	2	14910	15.75562	18.259068
CCTGGCCTTTGAACGCTAGACT	1665	0	1	11406	7.0146093	0.75884587
AGCTCACTGCAACCTCCGCCTC	1666	0	2	47293.5	20.812145	17.740503
GGGCAAGGAAACAGCCCCCA	1667	0	1	2351	7.9984035	-0.44823697
GGCTCTGTGTCTCCACCCAAAT	1668	0	1	3079	5.4224949	9.948535
TCACTGCAACCTCTGCCTCCCG	1669	0	2	43860.5	21.342369	14.672491
TCACCCCTCCATTCTCTCATGT	1670	0	1	3872	5.0523677	5.8481488
TGCTATGTTGCCAGGGTGGCC	1671	0	2	5818	7.5935292	5.3837776
AGCCCAATCCTAGCACTTTGAG	1672	0	2	2126.5	6.5217991	3.5096016

ROW# INFECTION NAME SEQ ID NOs OF GAMS ASSOCIATED WITH INFECTION

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- 2 B19 virus 11, 23, 28, 31, 36, 48, 66, 68, 73, 74, 85, 92, 105, 143, 144, 166, 177, 187, 216, 272, 279, 290, 293, 296, 299, 304, 315, 345, 346, 367, 380, 393, 418, 422, 433, 466, 467, 488, 492, 563, 564, 598, 610, 612, 619, 627, 637, 667, 681, 731, 746, 808, 838, 846, 855, 861, 879, 887, 891, 946, 947, 954, 973, 1009, 1012, 1053, 1065, 1078, 1128, 1133, 1161, 1163, 1166, 1172, 1174, 1181, 1186, 1195, 1206, 1270, 1273, 1299, 1303, 1328, 1348, 1363, 1385, 1406, 1442, 1469, 1486, 1520, 1523, 1547, 1579, 1594, 1642, 1670 and 119265-124793.
- 3 Barmah Forest virus 2, 11, 23, 31, 48, 49, 50, 68, 72, 73, 74, 82, 84, 85, 89, 92, 101, 105, 112, 131, 135, 143, 144, 166, 177, 198, 200, 201, 212, 216, 272, 277, 279, 290, 293, 296, 304, 315, 325, 330, 342, 345, 346, 364, 367, 377, 380, 393, 405, 418, 433, 466, 467, 479, 488, 492, 497, 503, 508, 529, 535, 563, 564, 566, 594, 595, 598, 601, 605, 610, 612, 619, 627, 637, 642, 658, 667, 694, 710, 712, 731, 746, 765, 808, 831, 838, 846, 855, 861, 882, 887, 891, 900, 945, 946, 947, 954, 973, 991, 1009, 1053, 1058, 1065, 1078, 1093, 1122, 1132, 1133, 1152, 1161, 1163, 1166, 1172, 1174, 1181, 1185, 1231, 1273, 1274, 1283, 1299, 1328, 1348, 1363, 1374, 1385, 1389, 1400, 1406, 1442, 1459, 1469, 1473, 1485, 1486, 1520, 1523, 1547, 1554, 1575, 1579, 1594, 1626, 1670 and 124794-128803.
- 4 BK polyomavirus 4, 11, 20, 23, 24, 29, 31, 35, 36, 37, 40, 43, 47, 48, 49, 50, 51, 66, 67, 70, 73, 74, 77, 78, 96, 114, 120, 143, 148, 169, 171, 174, 187, 188, 189, 200, 203, 212, 219, 231, 234, 239, 240, 244, 247, 252, 261, 262, 277, 279, 284, 286, 289, 290, 295, 303, 304, 310, 315, 321, 323, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 463, 465, 466, 481, 484, 500, 507, 509, 510, 515, 518, 526, 529, 537, 541, 544, 547, 551, 553, 561, 566, 567, 574, 575, 577, 579, 585, 587, 594, 605, 607, 610, 612, 617, 624, 625, 627, 635, 640, 652, 653, 654, 661, 663, 667, 676, 681, 684, 694, 696, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 832, 838, 839, 840, 846, 847, 854, 856, 862, 868, 872, 873, 876, 882, 886, 887, 889, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1019, 1020, 1037, 1038, 1040, 1049, 1050, 1058, 1062, 1065, 1069, 1070, 1084, 1086, 1090, 1096, 1101, 1106, 1123, 1129, 1133, 1138, 1139, 1144, 1152, 1153, 1159, 1163, 1168, 1172, 1190, 1195, 1196, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1321, 1328, 1330, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1456, 1459, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1505, 1507, 1511, 1526, 1549, 1552, 1574, 1578, 1579, 1580, 1584, 1586, 1598, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1642, 1643, 1654, 1656, 1665, 1669 and 128804-147105.
- 5 Bunyamwera virus 166, 323, 462, 478, 484, 541, 553, 559, 798, 867, 1057, 1063, 1069, 1484, 1560 and 147106-147728.
- 6 Colorado tick fever virus 20, 58, 64, 69, 88, 99, 103, 126, 130, 166, 186, 228, 245, 264, 286, 306, 319, 329, 330, 333, 346, 354, 361, 375, 386, 402, 418, 429, 451, 458, 470, 476, 502, 518, 520, 524, 527, 540, 548, 575, 584, 585, 611, 640, 677, 687, 691, 728, 732, 735, 774, 784, 803, 818, 847, 851, 876, 916, 932, 937, 940, 957, 959, 962, 964, 968, 1023, 1047, 1110, 1130, 1136, 1154, 1177, 1180, 1184, 1187, 1208, 1218, 1233, 1249, 1253, 1254, 1258, 1277, 1294, 1321, 1335, 1342, 1376, 1395, 1410,

- 1413, 1420, 1425, 1427, 1447, 1451, 1455, 1489, 1521, 1532, 1533, 1536, 1555, 1568, 1575, 1583, 1588, 1645, 1664 and 147729-148041.
- 7 Crimean-Congo hemorrhagic fever virus 1069, 1285, 1484, 1560 and 148042-149020.
- 8 Dengue virus 63, 64, 68, 166, 169, 196, 204, 229, 238, 271, 323, 376, 448, 462, 466, 478, 484, 541, 553, 559, 569, 570, 656, 657, 669, 798, 838, 853, 859, 867, 875, 935, 1005, 1057, 1063, 1069, 1239, 1285, 1308, 1358, 1372, 1373, 1386, 1400, 1402, 1484, 1560 and 149021-151652.
- 9 Dobrava virus 9, 63, 166, 271, 323, 462, 478, 484, 541, 553, 559, 569, 570, 798, 867, 951, 1057, 1063, 1069, 1285, 1484, 1560, 1581 and 151653-152681.
- 10 Eastern equine encephalitis virus 4, 5, 11, 20, 23, 24, 29, 31, 33, 35, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77, 78, 83, 84, 96, 99, 112, 114, 120, 129, 143, 145, 148, 154, 169, 171, 172, 174, 180, 187, 188, 189, 200, 203, 212, 219, 223, 224, 232, 234, 239, 240, 247, 252, 257, 261, 262, 268, 272, 277, 279, 283, 289, 290, 295, 303, 304, 306, 310, 315, 320, 321, 323, 334, 336, 337, 339, 347, 356, 357, 366, 370, 374, 376, 380, 386, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 465, 466, 467, 481, 483, 484, 500, 504, 507, 509, 510, 515, 518, 522, 526, 537, 541, 544, 547, 551, 553, 561, 562, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 617, 624, 627, 635, 637, 640, 652, 654, 661, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 774, 776, 777, 786, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 848, 854, 856, 862, 868, 873, 876, 882, 886, 889, 909, 911, 914, 924, 925, 927, 932, 935, 936, 938, 946, 954, 959, 960, 962, 966, 968, 969, 973, 977, 979, 985, 988, 998, 1006, 1008, 1019, 1020, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1069, 1070, 1084, 1086, 1090, 1096, 1101, 1105, 1106, 1115, 1123, 1124, 1129, 1133, 1138, 1139, 1152, 1153, 1159, 1163, 1168, 1172, 1190, 1196, 1204, 1205, 1212, 1219, 1225, 1229, 1234, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1281, 1284, 1290, 1293, 1297, 1299, 1305, 1306, 1321, 1328, 1330, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1374, 1383, 1390, 1391, 1392, 1408, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1456, 1459, 1460, 1467, 1469, 1473, 1474, 1476, 1481, 1485, 1487, 1488, 1499, 1503, 1507, 1511, 1526, 1537, 1549, 1551, 1552, 1574, 1578, 1579, 1580, 1584, 1606, 1617, 1624, 1627, 1631, 1633, 1637, 1639, 1640, 1643, 1644, 1654, 1656, 1661, 1665, 1669 and 152682-166891.
- 11 Hepatitis A virus 9, 23, 31, 36, 48, 78, 88, 105, 150, 162, 189, 203, 219, 229, 232, 233, 244, 248, 272, 278, 303, 306, 315, 325, 334, 351, 353, 365, 366, 373, 404, 416, 422, 429, 453, 458, 466, 467, 492, 520, 521, 541, 544, 561, 565, 571, 575, 581, 586, 597, 604, 614, 615, 619, 625, 641, 654, 661, 694, 713, 720, 736, 760, 778, 781, 802, 803, 820, 829, 839, 846, 875, 876, 877, 901, 909, 922, 973, 985, 989, 1006, 1009, 1012, 1019, 1035, 1036, 1047, 1062, 1065, 1069, 1092, 1116, 1129, 1130, 1134, 1144, 1157, 1166, 1172, 1180, 1185, 1195, 1197, 1199, 1205, 1216, 1227, 1251, 1258, 1266, 1268, 1287, 1293, 1299, 1304, 1328, 1332, 1335, 1338, 1351, 1363, 1371, 1373, 1392, 1394, 1406, 1429, 1437, 1469, 1486, 1488, 1550, 1554, 1557, 1594, 1598, 1611, 1619, 1631, 1637, 1640 and 166892-176205.
- 12 Hepatitis B virus 2, 6, 7, 8, 9, 10, 11, 13, 15, 19, 23, 24, 26, 28, 31, 36, 38, 47, 48, 50, 51, 54, 56, 57, 60, 66, 67, 68, 73, 74, 77, 78, 81, 83, 84, 85, 88, 92, 96, 101, 103, 105, 110, 114, 116, 127, 129, 130, 135, 139, 140, 142, 143, 144, 149, 150, 151, 154, 155, 158, 160, 162, 163, 166, 167, 169, 173, 174, 175, 177, 179, 182, 187, 189, 193, 194, 198, 199, 200, 202, 203, 204, 207, 208, 210, 212, 213, 216, 218, 219, 220, 221, 222, 225, 229, 230, 231, 232, 233, 234, 235, 236, 244, 247,

248, 249, 256, 261, 262, 263, 265, 272, 276, 278, 279, 280, 284, 286, 289, 290, 293, 295, 296, 298, 299, 302, 303, 304, 306, 307, 309, 312, 315, 318, 321, 323, 325, 331, 334, 336, 339, 344, 345, 346, 347, 351, 353, 356, 358, 359, 363, 365, 366, 367, 370, 372, 373, 374, 380, 382, 385, 387, 391, 393, 394, 396, 399, 400, 402, 404, 408, 409, 410, 412, 416, 418, 420, 422, 424, 425, 429, 433, 434, 435, 437, 443, 445, 446, 448, 453, 454, 457, 458, 460, 462, 463, 466, 467, 468, 469, 470, 471, 476, 478, 480, 481, 482, 484, 485, 486, 487, 488, 490, 492, 493, 499, 500, 505, 506, 509, 511, 516, 520, 521, 522, 526, 530, 531, 532, 534, 537, 539, 541, 542, 544, 545, 546, 551, 553, 555, 559, 561, 563, 564, 565, 566, 567, 569, 570, 572, 575, 579, 581, 583, 584, 585, 586, 590, 597, 598, 603, 604, 606, 610, 612, 614, 615, 618, 619, 623, 625, 627, 629, 635, 636, 637, 641, 643, 644, 645, 653, 654, 656, 661, 663, 666, 667, 668, 669, 671, 676, 679, 681, 684, 686, 688, 692, 693, 694, 698, 700, 703, 704, 707, 709, 711, 713, 715, 717, 720, 725, 731, 734, 736, 738, 744, 746, 750, 754, 760, 762, 765, 767, 778, 781, 783, 784, 786, 788, 795, 796, 797, 798, 801, 802, 803, 808, 809, 812, 813, 817, 820, 827, 829, 831, 832, 836, 838, 839, 846, 847, 848, 851, 854, 855, 857, 859, 861, 862, 867, 868, 872, 875, 876, 877, 879, 881, 882, 884, 886, 887, 889, 891, 894, 900, 901, 905, 908, 909, 910, 915, 918, 919, 920, 922, 924, 926, 927, 931, 932, 933, 935, 937, 938, 946, 947, 954, 960, 963, 965, 973, 975, 978, 980, 982, 983, 984, 985, 989, 990, 992, 993, 995, 998, 999, 1000, 1003, 1005, 1006, 1008, 1009, 1010, 1011, 1012, 1015, 1016, 1017, 1019, 1022, 1024, 1026, 1034, 1035, 1036, 1038, 1040, 1042, 1043, 1044, 1046, 1047, 1052, 1053, 1054, 1056, 1057, 1058, 1060, 1062, 1063, 1065, 1067, 1069, 1070, 1071, 1075, 1076, 1078, 1081, 1085, 1086, 1088, 1089, 1092, 1095, 1099, 1101, 1102, 1106, 1107, 1108, 1109, 1114, 1116, 1118, 1119, 1123, 1128, 1129, 1130, 1132, 1133, 1134, 1139, 1142, 1144, 1148, 1149, 1152, 1153, 1154, 1155, 1157, 1161, 1163, 1166, 1168, 1169, 1172, 1173, 1174, 1180, 1181, 1182, 1183, 1185, 1186, 1189, 1190, 1194, 1195, 1197, 1198, 1199, 1200, 1201, 1203, 1204, 1205, 1206, 1207, 1209, 1214, 1215, 1216, 1220, 1222, 1224, 1225, 1227, 1235, 1236, 1241, 1251, 1256, 1258, 1261, 1266, 1267, 1268, 1270, 1271, 1272, 1273, 1276, 1282, 1287, 1289, 1293, 1294, 1295, 1299, 1303, 1304, 1305, 1310, 1312, 1318, 1322, 1326, 1328, 1330, 1332, 1333, 1334, 1335, 1337, 1338, 1339, 1340, 1343, 1344, 1346, 1347, 1348, 1349, 1351, 1353, 1359, 1363, 1365, 1369, 1371, 1372, 1373, 1374, 1376, 1380, 1384, 1385, 1392, 1394, 1402, 1405, 1406, 1410, 1411, 1412, 1414, 1416, 1419, 1421, 1423, 1424, 1425, 1427, 1428, 1429, 1432, 1436, 1437, 1439, 1442, 1447, 1451, 1452, 1458, 1462, 1463, 1466, 1467, 1469, 1477, 1478, 1484, 1486, 1487, 1488, 1489, 1494, 1495, 1496, 1502, 1503, 1505, 1506, 1509, 1510, 1511, 1513, 1515, 1520, 1521, 1523, 1525, 1529, 1539, 1547, 1548, 1550, 1553, 1554, 1560, 1562, 1565, 1569, 1571, 1572, 1574, 1575, 1576, 1577, 1579, 1584, 1585, 1586, 1587, 1589, 1590, 1592, 1594, 1595, 1596, 1598, 1601, 1604, 1606, 1607, 1609, 1611, 1612, 1616, 1618, 1619, 1622, 1624, 1625, 1629, 1631, 1632, 1633, 1636, 1637, 1640, 1642, 1643, 1644, 1645, 1649, 1654, 1656, 1658, 1660, 1662, 1663, 1667, 1670 and 176206-229013.

13 Hepatitis C virus 2, 6, 7, 8, 9, 10, 11, 13, 14, 15, 19, 23, 24, 26, 28, 31, 36, 38, 40, 47, 48, 50, 51, 54, 56, 57, 60, 66, 67, 73, 74, 77, 78, 81, 84, 88, 101, 103, 105, 110, 114, 116, 127, 129, 130, 135, 139, 140, 142, 143, 149, 150, 151, 154, 155, 158, 160, 162, 163, 166, 167, 169, 173, 174, 175, 177, 179, 182, 187, 189, 193, 194, 199, 200, 203, 204, 207, 208, 209, 210, 212, 213, 218, 219, 220, 221, 222, 225, 229, 230, 231, 232, 233, 234, 235, 236, 244, 247, 248, 249, 256, 261, 262, 263, 265, 272, 276, 278, 279, 280, 286, 289, 290, 295, 298, 302, 303, 304, 306, 307,

309, 312, 315, 321, 323, 325, 328, 331, 334, 336, 339, 344, 345, 346, 351, 353, 356, 359, 363, 365, 366, 367, 370, 372, 373, 374, 380, 382, 385, 387, 391, 393, 394, 396, 399, 400, 404, 408, 409, 410, 412, 416, 420, 422, 424, 425, 429, 433, 434, 435, 437, 443, 445, 446, 448, 453, 454, 458, 460, 462, 466, 467, 468, 469, 470, 471, 476, 478, 480, 481, 482, 484, 485, 486, 490, 492, 493, 499, 500, 505, 506, 509, 511, 516, 520, 521, 522, 526, 530, 531, 532, 534, 537, 539, 541, 542, 544, 545, 546, 551, 553, 555, 559, 561, 564, 565, 566, 567, 569, 570, 572, 575, 581, 583, 584, 586, 590, 597, 598, 603, 604, 606, 610, 612, 614, 615, 618, 619, 623, 625, 627, 629, 635, 636, 641, 643, 645, 654, 656, 661, 666, 667, 668, 669, 671, 679, 684, 686, 688, 692, 693, 694, 698, 700, 703, 704, 707, 709, 711, 713, 715, 717, 720, 725, 731, 734, 736, 738, 744, 750, 754, 756, 760, 762, 765, 767, 778, 781, 783, 784, 786, 788, 795, 797, 798, 801, 802, 803, 804, 808, 809, 812, 813, 817, 820, 827, 829, 831, 832, 836, 838, 839, 846, 847, 848, 851, 855, 856, 857, 859, 861, 862, 867, 868, 872, 875, 876, 877, 879, 881, 882, 884, 886, 889, 894, 900, 901, 905, 908, 909, 910, 915, 919, 920, 922, 924, 926, 927, 931, 932, 933, 935, 937, 938, 946, 947, 960, 963, 965, 973, 975, 978, 980, 982, 983, 984, 985, 989, 990, 992, 993, 995, 998, 999, 1000, 1003, 1005, 1006, 1008, 1009, 1010, 1011, 1012, 1015, 1016, 1017, 1019, 1024, 1026, 1035, 1036, 1038, 1040, 1042, 1043, 1044, 1046, 1047, 1052, 1053, 1054, 1056, 1057, 1058, 1060, 1062, 1063, 1065, 1067, 1068, 1069, 1070, 1071, 1075, 1078, 1081, 1085, 1086, 1088, 1089, 1092, 1095, 1099, 1102, 1106, 1107, 1108, 1109, 1114, 1116, 1118, 1119, 1123, 1124, 1129, 1130, 1132, 1134, 1135, 1138, 1139, 1142, 1144, 1148, 1149, 1152, 1153, 1154, 1155, 1157, 1163, 1166, 1168, 1169, 1172, 1173, 1180, 1181, 1182, 1183, 1185, 1189, 1190, 1194, 1195, 1197, 1198, 1199, 1200, 1203, 1204, 1205, 1206, 1209, 1214, 1215, 1216, 1220, 1222, 1224, 1225, 1227, 1230, 1235, 1236, 1251, 1256, 1258, 1261, 1266, 1267, 1268, 1270, 1271, 1276, 1282, 1287, 1289, 1293, 1294, 1295, 1299, 1304, 1305, 1310, 1312, 1318, 1322, 1326, 1328, 1330, 1332, 1333, 1334, 1335, 1337, 1338, 1339, 1340, 1343, 1344, 1346, 1347, 1348, 1349, 1351, 1353, 1359, 1363, 1369, 1371, 1372, 1373, 1374, 1376, 1380, 1384, 1385, 1392, 1393, 1394, 1397, 1402, 1405, 1406, 1410, 1411, 1412, 1414, 1416, 1419, 1421, 1423, 1424, 1427, 1428, 1429, 1432, 1436, 1437, 1439, 1442, 1447, 1451, 1452, 1458, 1462, 1463, 1466, 1467, 1469, 1477, 1478, 1483, 1484, 1486, 1487, 1488, 1489, 1494, 1495, 1496, 1502, 1503, 1506, 1509, 1510, 1511, 1513, 1515, 1520, 1521, 1525, 1529, 1547, 1548, 1550, 1552, 1553, 1554, 1560, 1562, 1565, 1569, 1571, 1572, 1574, 1575, 1576, 1577, 1579, 1584, 1585, 1587, 1589, 1590, 1592, 1594, 1595, 1596, 1598, 1601, 1604, 1606, 1607, 1609, 1611, 1612, 1616, 1618, 1619, 1622, 1624, 1625, 1629, 1631, 1632, 1633, 1636, 1637, 1640, 1643, 1645, 1649, 1654, 1656, 1658, 1660, 1662, 1663, 1667, 1670, 1672 and 229014-279918.

14 Hepatitis D virus 2, 9, 15, 23, 26, 28, 31, 36, 48, 51, 78, 81, 88, 96, 105, 110, 139, 149, 150, 151, 162, 166, 173, 175, 189, 192, 202, 203, 204, 207, 213, 219, 229, 232, 233, 235, 244, 248, 249, 256, 272, 276, 278, 286, 289, 302, 303, 304, 306, 315, 318, 323, 325, 334, 339, 340, 346, 351, 353, 365, 366, 370, 373, 402, 404, 416, 422, 424, 429, 432, 437, 446, 448, 453, 458, 462, 466, 467, 470, 478, 480, 484, 486, 492, 500, 506, 520, 521, 522, 526, 541, 544, 553, 559, 561, 565, 575, 581, 586, 597, 600, 604, 610, 614, 615, 619, 625, 629, 635, 636, 641, 644, 645, 654, 661, 669, 679, 688, 692, 694, 700, 709, 713, 720, 734, 736, 750, 760, 762, 765, 767, 778, 781, 798, 802, 803, 820, 825, 827, 829, 839, 846, 847, 854, 867, 875, 876, 877, 894, 901, 909, 919, 922, 933, 935, 938, 963, 973, 975, 982, 985, 989, 995, 998, 1006, 1009, 1012, 1016, 1019, 1035, 1036, 1039, 1047, 1052, 1053, 1057,

1058, 1062, 1063, 1065, 1069, 1078, 1092, 1107, 1108, 1114, 1116, 1118, 1126, 1129, 1130, 1134, 1144, 1149, 1157, 1163, 1166, 1169, 1172, 1173, 1180, 1181, 1185, 1191, 1195, 1197, 1199, 1201, 1205, 1206, 1216, 1227, 1236, 1251, 1258, 1266, 1268, 1270, 1276, 1287, 1293, 1295, 1299, 1304, 1312, 1328, 1330, 1333, 1335, 1338, 1340, 1344, 1349, 1351, 1363, 1365, 1371, 1373, 1374, 1376, 1385, 1392, 1394, 1406, 1428, 1429, 1436, 1437, 1442, 1467, 1469, 1484, 1486, 1488, 1492, 1521, 1539, 1547, 1550, 1553, 1554, 1560, 1569, 1571, 1574, 1577, 1585, 1594, 1595, 1598, 1607, 1611, 1616, 1619, 1622, 1631, 1633, 1637, 1640, 1658, 1660, 1663 and 279919-296910.

15 Hepatitis E virus 7, 9, 23, 31, 36, 48, 78, 88, 92, 102, 105, 150, 162, 165, 166, 189, 192, 203, 218, 219, 223, 225, 229, 232, 233, 244, 248, 272, 278, 296, 303, 306, 315, 325, 334, 351, 353, 365, 366, 373, 401, 404, 416, 422, 429, 447, 453, 458, 459, 466, 467, 492, 520, 521, 541, 544, 560, 561, 565, 575, 581, 586, 597, 600, 604, 614, 615, 619, 625, 641, 654, 661, 694, 713, 720, 736, 760, 773, 778, 781, 802, 803, 818, 820, 829, 839, 846, 853, 855, 862, 875, 876, 877, 882, 895, 901, 909, 922, 928, 939, 973, 976, 985, 989, 997, 1006, 1009, 1012, 1019, 1035, 1036, 1042, 1047, 1062, 1065, 1069, 1092, 1116, 1129, 1130, 1134, 1139, 1144, 1157, 1163, 1166, 1172, 1180, 1185, 1195, 1197, 1199, 1201, 1205, 1216, 1224, 1227, 1251, 1258, 1266, 1268, 1270, 1287, 1293, 1298, 1299, 1304, 1318, 1328, 1335, 1336, 1338, 1345, 1346, 1351, 1356, 1363, 1371, 1373, 1392, 1394, 1406, 1429, 1437, 1439, 1444, 1469, 1486, 1488, 1508, 1550, 1554, 1594, 1597, 1598, 1610, 1611, 1619, 1631, 1637, 1640, 1647, 1648, 1667 and 296911-304515.

16 Human adenovirus A 4, 11, 16, 20, 23, 24, 29, 31, 35, 36, 37, 40, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77, 78, 96, 102, 114, 120, 143, 148, 151, 154, 169, 171, 174, 187, 188, 189, 197, 200, 203, 212, 216, 219, 231, 234, 239, 240, 247, 248, 252, 261, 262, 271, 276, 277, 279, 284, 286, 289, 290, 295, 303, 304, 310, 315, 321, 323, 329, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 383, 394, 395, 396, 399, 400, 401, 405, 413, 416, 421, 424, 429, 431, 433, 437, 441, 443, 446, 450, 453, 454, 460, 462, 463, 465, 466, 481, 484, 485, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 551, 553, 561, 566, 567, 574, 575, 577, 579, 585, 587, 594, 605, 607, 610, 612, 617, 624, 625, 627, 635, 640, 652, 653, 654, 656, 661, 663, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 750, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 836, 838, 839, 840, 846, 847, 854, 856, 862, 868, 873, 876, 882, 886, 889, 909, 911, 914, 920, 924, 925, 927, 929, 934, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1019, 1020, 1035, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1068, 1069, 1070, 1078, 1079, 1084, 1086, 1090, 1096, 1101, 1106, 1123, 1129, 1133, 1138, 1139, 1142, 1144, 1146, 1152, 1153, 1155, 1159, 1163, 1168, 1172, 1190, 1195, 1196, 1198, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1315, 1321, 1328, 1330, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1393, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1456, 1459, 1460, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1505, 1507, 1511, 1526, 1549, 1552, 1574, 1578, 1579, 1580, 1584, 1586, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1642, 1643, 1645, 1654, 1656, 1665, 1669 and 304516-323838.

17 Human adenovirus B (1, 25, 33, 51, 52, 60, 81, 91, 103, 111, 126, 129, 131, 151, 157, 162, 164, 167, HAdV-B) 180, 183, 186, 210, 222, 247, 270, 302, 307, 309, 310, 324, 326, 349, 373, 383, 430, 434, 439, 442, 461, 473, 474, 486, 494, 505, 527, 529, 530, 531, 533, 545, 563, 571, 576, 582, 634, 657, 660, 714, 775, 795, 804, 807, 813, 850, 858, 871,

872, 893, 923, 957, 960, 981, 1001, 1011, 1022, 1042, 1046, 1063, 1066, 1074, 1075, 1083, 1093, 1115, 1126, 1133, 1143, 1209, 1214, 1223, 1229, 1261, 1292, 1315, 1316, 1337, 1346, 1352, 1353, 1375, 1391, 1405, 1408, 1411, 1423, 1425, 1443, 1475, 1489, 1490, 1496, 1498, 1517, 1540, 1545, 1568, 1577, 1593, 1596, 1606, 1610, 1632, 1642, 1643, 1654, 1664 and 325308-325714.

18 Human adenovirus C 1, 7, 17, 26, 33, 36, 44, 46, 50, 60, 69, 73, 84, 89, 90, 91, 95, 97, 100, 103, 111, 112, 115, 117, 121, 125, 129, 136, 140, 141, 143, 144, 149, 150, 151, 164, 165, 167, 169, 174, 183, 186, 191, 192, 200, 201, 202, 203, 212, 216, 219, 228, 237, 242, 247, 248, 250, 256, 257, 264, 265, 268, 271, 275, 286, 287, 292, 294, 296, 301, 302, 303, 309, 311, 314, 316, 320, 321, 323, 325, 327, 333, 334, 343, 347, 362, 367, 370, 373, 376, 380, 382, 384, 385, 386, 389, 392, 397, 403, 406, 408, 411, 414, 418, 421, 424, 437, 441, 442, 445, 447, 450, 451, 455, 459, 468, 472, 474, 475, 477, 479, 480, 485, 486, 489, 490, 493, 494, 495, 499, 505, 510, 518, 525, 526, 532, 533, 541, 542, 544, 545, 552, 553, 563, 566, 567, 568, 572, 582, 584, 587, 591, 593, 599, 600, 611, 616, 618, 623, 626, 629, 632, 648, 656, 658, 660, 661, 663, 670, 674, 677, 679, 680, 685, 690, 691, 694, 697, 699, 702, 707, 714, 716, 720, 721, 732, 733, 736, 742, 743, 746, 749, 750, 752, 759, 760, 765, 769, 770, 775, 778, 779, 781, 783, 784, 785, 786, 794, 795, 796, 799, 804, 805, 809, 813, 819, 825, 829, 839, 842, 843, 848, 851, 856, 862, 870, 874, 880, 883, 886, 888, 893, 900, 901, 903, 912, 918, 919, 920, 924, 928, 929, 932, 933, 934, 935, 939, 940, 947, 948, 955, 956, 958, 960, 966, 974, 976, 977, 978, 979, 980, 987, 990, 993, 996, 997, 999, 1002, 1012, 1015, 1018, 1025, 1028, 1035, 1038, 1039, 1047, 1049, 1051, 1055, 1058, 1062, 1067, 1069, 1072, 1073, 1075, 1076, 1078, 1081, 1084, 1085, 1093, 1094, 1101, 1102, 1104, 1109, 1113, 1115, 1121, 1126, 1127, 1128, 1129, 1131, 1139, 1141, 1142, 1152, 1153, 1154, 1157, 1163, 1166, 1167, 1170, 1177, 1186, 1191, 1194, 1197, 1201, 1204, 1207, 1209, 1214, 1218, 1226, 1227, 1233, 1239, 1246, 1253, 1255, 1257, 1265, 1270, 1281, 1283, 1287, 1289, 1300, 1305, 1307, 1308, 1310, 1315, 1318, 1320, 1321, 1324, 1327, 1329, 1330, 1331, 1332, 1333, 1336, 1340, 1344, 1348, 1353, 1355, 1356, 1358, 1360, 1367, 1370, 1375, 1376, 1379, 1382, 1391, 1399, 1404, 1405, 1406, 1408, 1410, 1411, 1412, 1421, 1423, 1427, 1433, 1436, 1438, 1439, 1442, 1444, 1447, 1454, 1455, 1458, 1466, 1467, 1469, 1478, 1480, 1489, 1490, 1492, 1498, 1499, 1504, 1509, 1510, 1519, 1521, 1527, 1528, 1535, 1538, 1541, 1555, 1575, 1577, 1582, 1583, 1585, 1586, 1592, 1600, 1626, 1628, 1629, 1631, 1633, 1634, 1636, 1642, 1648, 1650, 1651, 1652, 1653, 1657, 1664, 1665, 1666, 1667 and 326939-329044.

19 Human adenovirus D 1, 4, 5, 8, 9, 12, 17, 19, 21, 23, 25, 26, 33, 36, 40, 41, 44, 45, 46, 51, 52, 58, 65, 69, 71, 73, 74, 80, 81, 84, 89, 91, 93, 97, 99, 102, 103, 111, 112, 115, 117, 121, 123, 124, 125, 126, 128, 130, 133, 137, 143, 145, 148, 149, 151, 162, 164, 167, 169, 172, 174, 182, 183, 186, 192, 194, 196, 199, 200, 201, 203, 206, 210, 216, 217, 218, 219, 222, 223, 225, 228, 232, 240, 247, 248, 250, 252, 256, 257, 264, 265, 267, 268, 272, 273, 279, 283, 286, 289, 290, 292, 296, 297, 301, 302, 303, 309, 316, 321, 323, 324, 325, 332, 334, 342, 343, 350, 352, 357, 361, 363, 365, 367, 370, 373, 375, 384, 392, 397, 401, 406, 407, 412, 418, 420, 421, 423, 424, 432, 434, 438, 439, 442, 444, 447, 450, 455, 467, 468, 469, 474, 484, 485, 486, 490, 493, 495, 496, 499, 503, 504, 505, 510, 513, 514, 518, 544, 545, 548, 553, 559, 563, 566, 567, 572, 579, 582, 586, 587, 589, 591, 593, 599, 600, 601, 613, 616, 617, 618, 623, 632, 634, 642, 645, 648, 656, 660, 661, 662, 664, 667, 670, 690, 694, 695, 696, 697, 702, 714, 719, 724, 736, 738, 742, 744, 750, 765, 766, 770, 778, 779, 781, 785, 786, 790, 795, 798, 799, 806, 809, 810, 819,

826, 829, 839, 842, 843, 847, 848, 850, 851, 852, 860, 861, 868, 872, 874, 879, 880, 882, 888, 892, 895, 897, 903, 911, 928, 929, 933, 934, 935, 940, 947, 948, 956, 957, 960, 966, 974, 975, 977, 978, 979, 980, 987, 991, 997, 999, 1001, 1004, 1009, 1011, 1012, 1015, 1018, 1022, 1028, 1029, 1035, 1039, 1040, 1043, 1046, 1047, 1048, 1049, 1053, 1058, 1062, 1063, 1069, 1072, 1075, 1076, 1078, 1079, 1080, 1083, 1088, 1093, 1101, 1102, 1109, 1112, 1115, 1121, 1126, 1128, 1129, 1133, 1139, 1142, 1143, 1146, 1152, 1153, 1155, 1162, 1163, 1164, 1177, 1181, 1188, 1191, 1192, 1194, 1199, 1201, 1204, 1208, 1209, 1219, 1223, 1225, 1227, 1228, 1231, 1239, 1240, 1245, 1247, 1250, 1257, 1258, 1259, 1263, 1265, 1276, 1277, 1282, 1287, 1289, 1292, 1295, 1298, 1300, 1307, 1308, 1309, 1310, 1311, 1316, 1318, 1320, 1321, 1328, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1340, 1341, 1342, 1345, 1348, 1355, 1356, 1358, 1375, 1376, 1379, 1391, 1395, 1404, 1405, 1406, 1410, 1411, 1414, 1419, 1421, 1423, 1425, 1426, 1427, 1436, 1439, 1443, 1444, 1447, 1454, 1455, 1458, 1466, 1467, 1469, 1475, 1476, 1480, 1489, 1492, 1493, 1498, 1499, 1508, 1509, 1510, 1515, 1519, 1521, 1523, 1528, 1533, 1535, 1536, 1537, 1538, 1540, 1549, 1575, 1579, 1581, 1582, 1585, 1597, 1600, 1602, 1628, 1631, 1632, 1642, 1643, 1647, 1648, 1651, 1652, 1661, 1664 and 329045-331119.

20 Human adenovirus E 4, 19, 32, 33, 36, 44, 51, 58, 61, 71, 74, 81, 84, 91, 93, 95, 97, 103, 107, 115, 126, 127, 128, 129, 137, 140, 141, 145, 149, 151, 164, 165, 169, 172, 174, 182, 183, 191, 192, 200, 203, 206, 210, 216, 218, 220, 222, 223, 227, 228, 231, 232, 247, 248, 252, 253, 256, 260, 264, 268, 271, 275, 279, 288, 291, 294, 297, 301, 303, 304, 307, 309, 321, 324, 326, 329, 334, 342, 343, 349, 350, 357, 361, 364, 365, 367, 370, 373, 376, 384, 385, 386, 392, 403, 406, 408, 412, 414, 416, 421, 423, 424, 429, 434, 437, 439, 441, 444, 447, 449, 455, 459, 464, 468, 469, 478, 484, 485, 486, 490, 493, 494, 495, 496, 497, 499, 502, 503, 504, 505, 513, 524, 532, 533, 541, 544, 548, 553, 560, 563, 566, 567, 575, 577, 582, 584, 585, 586, 587, 589, 591, 599, 600, 601, 608, 613, 614, 615, 616, 618, 632, 634, 636, 643, 645, 648, 649, 656, 660, 661, 667, 670, 690, 693, 695, 697, 702, 714, 721, 722, 725, 746, 749, 750, 762, 765, 769, 770, 779, 780, 781, 786, 792, 795, 799, 803, 806, 813, 819, 821, 829, 834, 839, 842, 843, 847, 848, 850, 860, 862, 868, 872, 874, 880, 882, 886, 895, 897, 911, 919, 928, 929, 932, 933, 934, 935, 939, 940, 946, 947, 948, 960, 962, 979, 981, 987, 993, 996, 997, 999, 1001, 1002, 1012, 1022, 1035, 1039, 1040, 1042, 1043, 1046, 1047, 1049, 1051, 1053, 1058, 1062, 1063, 1067, 1069, 1072, 1073, 1076, 1077, 1078, 1083, 1088, 1102, 1104, 1109, 1112, 1115, 1126, 1127, 1129, 1133, 1139, 1142, 1146, 1152, 1153, 1163, 1164, 1177, 1181, 1191, 1192, 1194, 1197, 1201, 1202, 1204, 1206, 1208, 1209, 1212, 1219, 1225, 1228, 1229, 1239, 1247, 1249, 1250, 1254, 1263, 1269, 1274, 1277, 1287, 1292, 1307, 1310, 1318, 1320, 1321, 1324, 1330, 1331, 1336, 1337, 1340, 1341, 1353, 1356, 1358, 1360, 1363, 1375, 1376, 1391, 1398, 1400, 1403, 1405, 1410, 1411, 1416, 1419, 1421, 1430, 1436, 1439, 1443, 1444, 1454, 1455, 1458, 1466, 1470, 1474, 1478, 1480, 1489, 1492, 1495, 1498, 1499, 1521, 1523, 1526, 1530, 1532, 1535, 1537, 1538, 1540, 1560, 1572, 1578, 1579, 1588, 1597, 1598, 1600, 1602, 1610, 1613, 1624, 1628, 1631, 1632, 1642, 1643, 1647, 1648, 1665, 1667 and 331120-332804.

21 Human adenovirus F 5, 9, 19, 25, 33, 36, 40, 44, 46, 49, 50, 52, 61, 69, 74, 81, 82, 84, 88, 97, 99, 115, 119, 131, 136, 141, 145, 151, 164, 167, 169, 172, 183, 186, 191, 192, 196, 199, 202, 210, 216, 218, 220, 222, 226, 235, 242, 245, 247, 252, 256, 257, 259, 274, 279, 288, 292, 303, 307, 309, 316, 319, 320, 323, 325, 326, 337, 343, 344, 350, 357, 364, 370, 373, 376, 378, 383, 403, 406, 408, 409, 420, 421, 423,

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22 Human astrovirus 197, 450, 466, 954, 1198 and 334516-335246.

23 Human coronavirus 22 36, 120, 173, 197, 201, 225, 231, 233, 276, 284, 286, 290, 347, 356, 388, 389, 9E 404, 408, 450, 454, 461, 463, 466, 488, 544, 545, 548, 566, 579, 585, 616, 625, 643, 653, 663, 676, 694, 712, 768, 813, 831, 839, 855, 868, 887, 894, 909, 920, 954, 959, 980, 1029, 1033, 1062, 1079, 1085, 1092, 1101, 1118, 1138, 1139, 1140, 1144, 1153, 1163, 1168, 1172, 1173, 1187, 1190, 1195, 1198, 1208, 1222, 1258, 1259, 1293, 1315, 1325, 1335, 1346, 1396, 1430, 1431, 1442, 1469, 1471, 1505, 1522, 1551, 1585, 1586, 1593, 1642 and 335247-340599.

24 Human coronavirus OC 132, 545, 563, 1195, 1292, 1522 and 340600-340686.
43 (HCoV-OC43)

25 Human echovirus 1 4, 11, 20, 23, 24, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 66, 67, 68, 70, 73, 74, 77, 78, 85, 92, 96, 105, 114, 120, 143, 144, 148, 154, 166, 169, 171, 174, 177, 187, 188, 189, 200, 203, 212, 216, 219, 229, 231, 234, 239, 240, 247, 252, 261, 262, 272, 276, 277, 279, 284, 286, 289, 290, 293, 295, 296, 303, 304, 310, 315, 321, 323, 334, 336, 339, 345, 346, 347, 353, 356, 357, 366, 367, 370, 374, 376, 380, 393, 394, 395, 396, 399, 400, 401, 405, 413, 416, 418, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 463, 465, 466, 467, 481, 484, 488, 492, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 548, 551, 553, 561, 563, 564, 566, 567, 574, 575, 577, 579, 585, 587, 594, 598, 605, 607, 610, 612, 614, 616, 617, 619, 624, 625, 627, 635, 637, 640, 641, 643, 652, 653, 654, 661, 663, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 808, 811, 813, 829, 838, 839, 840, 846, 847, 854, 855, 856, 861, 862, 868, 873, 876, 882, 886, 887, 889, 891, 894, 901, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 946, 947, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1009, 1019, 1020, 1029, 1037, 1038, 1040, 1047, 1049, 1053, 1058, 1062, 1065, 1069, 1070, 1078, 1079, 1084, 1086, 1090, 1092, 1096, 1101, 1106, 1118, 1123, 1129, 1133, 1134, 1138, 1139, 1140, 1144, 1152, 1153, 1159, 1161, 1163, 1166, 1168, 1172, 1173, 1174, 1181, 1185, 1187, 1190, 1195, 1196, 1199, 1204, 1205, 1208, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1273, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1315, 1321, 1325, 1328, 1330, 1332,

1335, 1338, 1339, 1348, 1349, 1351, 1353, 1363, 1364, 1373, 1385, 1390, 1391, 1392, 1406, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1442, 1456, 1459, 1467, 1469, 1471, 1473, 1476, 1481, 1485, 1486, 1487, 1488, 1503, 1505, 1507, 1511, 1520, 1523, 1526, 1547, 1549, 1552, 1557, 1574, 1578, 1579, 1580, 1584, 1585, 1586, 1594, 1598, 1606, 1611, 1617, 1631, 1633, 1637, 1639, 1640, 1642, 1643, 1654, 1656, 1665, 1669, 1670 and 345885-370019.

- 26 Human enterovirus A 4, 11, 20, 23, 24, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 66, 67, 68, 70, 73, 74, 77, 78, 85, 92, 96, 105, 114, 120, 143, 144, 148, 154, 166, 169, 171, 174, 177, 187, 188, 189, 200, 203, 212, 216, 219, 229, 231, 234, 239, 240, 247, 252, 261, 262, 272, 276, 277, 279, 284, 286, 289, 290, 293, 295, 296, 303, 304, 310, 315, 321, 323, 334, 336, 339, 345, 346, 347, 353, 356, 357, 366, 367, 370, 374, 376, 380, 393, 394, 395, 396, 399, 400, 401, 405, 413, 416, 418, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 463, 465, 466, 467, 481, 484, 488, 492, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 548, 551, 553, 561, 563, 564, 566, 567, 574, 575, 577, 579, 585, 587, 594, 598, 605, 607, 610, 612, 614, 616, 617, 619, 624, 625, 627, 635, 637, 640, 641, 643, 652, 653, 654, 661, 663, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 808, 811, 813, 829, 838, 839, 840, 846, 847, 854, 855, 856, 861, 862, 868, 873, 876, 882, 886, 887, 889, 891, 894, 901, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 946, 947, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1009, 1019, 1020, 1029, 1037, 1038, 1040, 1047, 1049, 1053, 1058, 1062, 1065, 1069, 1070, 1078, 1079, 1084, 1086, 1090, 1092, 1096, 1101, 1106, 1118, 1123, 1129, 1133, 1134, 1138, 1139, 1140, 1144, 1152, 1153, 1159, 1161, 1163, 1166, 1168, 1172, 1173, 1174, 1181, 1185, 1187, 1190, 1195, 1196, 1199, 1204, 1205, 1208, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1273, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1315, 1321, 1325, 1328, 1330, 1332, 1335, 1338, 1339, 1348, 1349, 1351, 1353, 1363, 1364, 1373, 1385, 1390, 1391, 1392, 1406, 1411, 1412, 1416, 1423, 1424, 1426, 1431, 1432, 1442, 1456, 1459, 1467, 1469, 1471, 1473, 1476, 1481, 1485, 1486, 1487, 1488, 1503, 1505, 1507, 1511, 1520, 1523, 1526, 1547, 1549, 1552, 1557, 1574, 1578, 1579, 1580, 1584, 1585, 1586, 1594, 1598, 1606, 1611, 1617, 1631, 1633, 1637, 1639, 1640, 1642, 1643, 1654, 1656, 1665, 1669, 1670 and 370020-394641.
- 27 Human enterovirus B 466, 876, 1332, 1431, 1557 and 394642-397190.
- 28 Human enterovirus C 466, 876, 1332, 1431, 1557 and 397191-399739.
- 29 Human enterovirus D 36, 231, 284, 286, 347, 356, 463, 466, 544, 566, 579, 585, 625, 653, 663, 676, 694, 839, 876, 909, 920, 980, 1062, 1101, 1144, 1195, 1258, 1293, 1332, 1335, 1431, 1469, 1505, 1557, 1586 and 399740-404272.
- 30 Human enterovirus E 466, 876, 1332, 1431, 1557 and 404273-406821.
- 31 Human erythrovirus V 28, 36, 66, 187, 299, 422, 681, 1128, 1186, 1195, 1206, 1270, 1303, 1642 and 406822-408538.
- 32 Human herpesvirus 1 1, 4, 9, 11, 12, 17, 19, 20, 21, 23, 24, 29, 31, 33, 35, 37, 40, 43, 45, 47, 48, 49, 51, 54, 58, 60, 61, 66, 67, 68, 69, 70, 73, 74, 77, 78, 80, 84, 85, 88, 89, 92, 93, 95, 96, 101, 102, 105, 114, 115, 117, 119, 120, 123, 128, 130, 136, 141, 143, 144, 148, 154, 166, 167, 169, 171, 172, 174, 177, 182, 183, 186, 187, 188, 189, 191, 192, 196, 200, 201, 202, 203, 206, 210, 212, 216, 217, 218, 219, 220, 222, 223, 227, 229, 231, 234, 235, 239, 240, 247, 248, 250, 252, 255, 256, 257, 259, 261, 262, 264, 267, 272, 277, 279, 282, 284, 286, 287, 288, 289, 290, 291, 292, 293, 295, 296, 297, 301, 303, 304, 310, 314, 315, 316, 321, 322, 323, 324, 326, 332, 334, 336, 339, 340, 343, 345, 346, 347, 349, 351, 352, 353, 355, 356,

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33 Human herpesvirus 10 6, 19, 20, 23, 24, 29, 31, 34, 48, 50, 51, 67, 69, 70, 73, 74, 77, 78, 104, 112, 114, 116, 120, 121, 141, 143, 151, 167, 174, 177, 179, 188, 204, 212, 219, 223, 231, 234, 239, 240, 247, 259, 276, 277, 279, 288, 290, 298, 303, 304, 306, 310, 315, 323, 334, 336, 339, 345, 351, 366, 367, 370, 380, 384, 385, 394, 396, 399, 400, 401, 410, 413, 422, 423, 424, 429, 431, 433, 452, 454, 462, 466, 478, 480, 481, 484, 500, 509, 510, 515, 518, 526, 544, 546, 561, 564, 568, 569, 572, 575, 576, 577, 582, 587, 598, 607, 609, 610, 612, 617, 624, 625, 627, 640, 643, 651, 652, 654, 661, 667, 674, 676, 681, 684, 688, 693, 710, 713, 720, 725, 731, 734, 737, 746, 749, 750, 754, 760, 770, 772, 777, 784, 795, 803, 812, 813, 816, 829,

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- 34 Human herpesvirus 2 4, 5, 9, 11, 12, 17, 19, 20, 23, 24, 29, 31, 33, 35, 37, 43, 47, 48, 49, 51, 54, 58, 59, 66, 67, 68, 70, 73, 74, 77, 78, 84, 85, 88, 89, 90, 91, 92, 93, 96, 101, 102, 105, 114, 117, 120, 127, 128, 129, 140, 143, 144, 145, 148, 151, 152, 154, 155, 162, 164, 166, 167, 169, 171, 174, 176, 177, 178, 182, 184, 185, 187, 188, 189, 192, 194, 196, 200, 203, 206, 210, 211, 212, 216, 217, 218, 219, 222, 223, 228, 229, 231, 232, 234, 235, 237, 239, 240, 245, 247, 250, 252, 253, 255, 256, 257, 259, 261, 262, 264, 267, 270, 272, 275, 277, 279, 284, 286, 287, 289, 290, 291, 292, 293, 294, 295, 296, 299, 303, 304, 306, 307, 310, 314, 315, 321, 323, 324, 325, 330, 332, 334, 335, 336, 339, 340, 343, 345, 346, 347, 350, 351, 352, 353, 356, 357, 362, 363, 365, 366, 367, 370, 374, 375, 376, 377, 378, 380, 381, 383, 385, 387, 393, 394, 395, 396, 397, 399, 400, 401, 403, 405, 406, 409, 412, 413, 416, 418, 420, 421, 423, 424, 429, 430, 431, 432, 433, 434, 437, 438, 439, 440, 441, 443, 446, 447, 448, 451, 453, 454, 457, 458, 462, 463, 465, 466, 467, 470, 472, 480, 481, 483, 484, 488, 490, 492, 493, 495, 496, 499, 500, 504, 505, 507, 509, 510, 514, 515, 518, 520, 524, 526, 527, 532, 533, 535, 537, 541, 543, 544, 547, 548, 550, 551, 553, 554, 555, 559, 560, 561, 562, 563, 564, 566, 567, 572, 574, 575, 577, 579, 582, 584, 585, 587, 591, 593, 594, 598, 599, 600, 605, 607, 610, 611, 612, 613, 614, 615, 617, 618, 619, 624, 625, 626, 627, 632, 635, 637, 640, 641, 642, 648, 652, 653, 654, 655, 660, 661, 663, 667, 670, 674, 676, 681, 684, 685, 687, 693, 695, 697, 701, 702, 703, 709, 710, 712, 713, 714, 715, 719, 720, 721, 731, 734, 736, 737, 746, 749, 750, 754, 756, 760, 763, 773, 776, 777, 779, 780, 783, 786, 796, 798, 799, 801, 802, 803, 804, 805, 808, 811, 812, 813, 815, 819, 821, 822, 826, 829, 836, 838, 839, 840, 843, 845, 846, 847, 848, 853, 854, 855, 856, 860, 861, 862, 868, 869, 873, 874, 876, 879, 882, 886, 887, 889, 890, 891, 892, 901, 909, 911, 912, 914, 916, 919, 920, 921, 924, 925, 927, 929, 933, 934, 935, 936, 937, 938, 945, 946, 947, 948, 954, 956, 959, 960, 962, 966, 969, 973, 976, 977, 979, 980, 981, 985, 988, 990, 993, 994, 997, 998, 999, 1001, 1002, 1006, 1008, 1009, 1012, 1018, 1019, 1020, 1022, 1023, 1026, 1032, 1033, 1035, 1037, 1038, 1039, 1040, 1043, 1046, 1047, 1049, 1051, 1053, 1055, 1058, 1062, 1065, 1069, 1070, 1072, 1073, 1075, 1076, 1078, 1081, 1083, 1084, 1086, 1088, 1090, 1091, 1096, 1101, 1102, 1103, 1104, 1106, 1112, 1118, 1120, 1121, 1122, 1123, 1128, 1129, 1130, 1131, 1133, 1134, 1136, 1137, 1138, 1139, 1144, 1146, 1152, 1153, 1157, 1158, 1159, 1161, 1162, 1163, 1166, 1167, 1168, 1172, 1174, 1177, 1179, 1180, 1181, 1185, 1190, 1191, 1192, 1194, 1195, 1196, 1197, 1199, 1204, 1205, 1208, 1212, 1214, 1219, 1222, 1225, 1226, 1227, 1228, 1230, 1239, 1245, 1250, 1251, 1254, 1255, 1257, 1258, 1262, 1268, 1270, 1271, 1273, 1274, 1284, 1289, 1290, 1293, 1297, 1298, 1299, 1300, 1301, 1305, 1306, 1307, 1316, 1318, 1319, 1321, 1324, 1328, 1330, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1344, 1348, 1349, 1351, 1353, 1356, 1360, 1363, 1364, 1367, 1373, 1375, 1379, 1383, 1385, 1389, 1390, 1391, 1392, 1399, 1400, 1403, 1406, 1411,

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35 Human herpesvirus 3 4, 9, 11, 18, 19, 20, 23, 24, 29, 31, 35, 37, 43, 45, 47, 48, 49, 51, 54, 59,

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36 Human herpesvirus 4 19, 24, 29, 33, 51, 60, 74, 77, 81, 93, 97, 99, 117, 118, 121, 126, 127, 129, (Epstein-Barr virus) 130, 131, 133, 148, 151, 155, 162, 164, 167, 169, 183, 186, 189, 198, 203, 210,

212, 222, 223, 231, 234, 240, 247, 250, 253, 267, 270, 279, 290, 291, 302, 304, 307, 310, 314, 324, 326, 332, 336, 342, 347, 349, 352, 367, 370, 373, 376, 382, 383, 384, 392, 406, 412, 423, 424, 429, 432, 441, 442, 447, 461, 476, 493, 494, 502, 505, 517, 529, 530, 532, 533, 545, 548, 553, 563, 571, 575, 584, 587, 598, 602, 604, 614, 632, 636, 643, 645, 654, 657, 673, 677, 690, 691, 696, 697, 733, 735, 746, 770, 771, 779, 784, 792, 795, 798, 801, 803, 808, 813, 819, 825, 847, 858, 861, 863, 872, 877, 919, 923, 942, 947, 960, 978, 981, 990, 997, 999, 1011,

1012, 1015, 1022, 1023, 1038, 1039, 1042, 1046, 1051, 1052, 1053, 1063, 1067, 1075, 1083, 1085, 1086, 1090, 1092, 1120, 1126, 1128, 1129, 1131, 1133, 1139, 1146, 1154, 1163, 1166, 1179, 1184, 1188, 1194, 1195, 1201, 1205, 1209, 1223, 1224, 1226, 1228, 1241, 1245, 1264, 1269, 1285, 1287, 1289, 1293, 1295, 1298, 1305, 1308, 1315, 1316, 1330, 1337, 1341, 1352, 1356, 1359, 1360, 1363, 1375, 1378, 1382, 1387, 1391, 1394, 1404, 1405, 1406, 1408, 1410, 1411, 1412, 1423, 1425, 1443, 1444, 1451, 1458, 1466, 1467, 1485, 1489, 1490, 1493, 1495, 1501, 1509, 1517, 1526, 1528, 1538, 1545, 1566, 1577, 1583, 1593, 1596, 1600, 1610, 1627, 1632, 1633, 1642, 1643, 1645, 1650, 1653, 1664, 1669 and 489882-493677.

37 Human herpesvirus 5 1, 2, 4, 6, 7, 9, 11, 13, 17, 19, 20, 21, 23, 24, 27, 29, 31, 35, 36, 37, 40, 41, 43, 45, 47, 48, 49, 50, 51, 63, 64, 66, 67, 68, 69, 70, 71, 72, 73, 74, 77, 78, 83, 85, 86, 88, 92, 93, 95, 96, 97, 99, 100, 105, 112, 114, 120, 121, 123, 127, 128, 129, 130, 133, 134, 140, 141, 143, 144, 148, 149, 150, 152, 154, 156, 159, 162, 164, 165, 166, 167, 168, 169, 171, 172, 174, 176, 177, 179, 180, 181, 182, 184, 186, 187, 188, 189, 192, 195, 196, 200, 201, 202, 203, 204, 206, 207, 209, 210, 211, 212, 216, 217, 218, 219, 220, 222, 227, 228, 229, 231, 232, 233, 234, 235, 238, 239, 240, 247, 250, 251, 252, 253, 254, 255, 256, 259, 261, 262, 264, 265, 271, 272, 274, 276, 277, 279, 284, 286, 289, 290, 292, 293, 294, 295, 296, 297, 301, 302, 303, 304, 309, 310, 311, 314, 315, 316, 317, 319, 321, 323, 325, 326, 327, 332, 334, 336, 339, 340, 342, 345, 346, 347, 348, 349, 350, 353, 356, 357, 360, 361, 362, 363, 366, 367, 368, 369, 370, 373, 374, 376, 380, 381, 382, 386, 387, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 404, 405, 406, 407, 410, 412, 413, 415, 416, 418, 419, 423, 424, 429, 431, 433, 437, 440, 441, 443, 444, 446, 447, 448, 451, 452, 453, 454, 456, 458, 459, 462, 463, 464, 465, 466, 467, 468, 469, 472, 476, 477, 478, 481, 482, 484, 485, 488, 490, 492, 493, 495, 496, 500, 504, 505, 507, 508, 509, 510, 511, 515, 518, 520, 521, 523, 524, 526, 530, 532, 533, 535, 537, 540, 541, 543, 544, 545, 547, 548, 550, 551, 552, 553, 555, 559, 560, 561, 562, 563, 564, 566, 567, 569, 570, 572, 574, 575, 577, 578, 579, 582, 585, 586, 587, 594, 596, 597, 598, 600, 604, 605, 607, 610, 612, 613, 614, 615, 616, 617, 618, 619, 624, 625, 626, 627, 632, 634, 635, 636, 637, 640, 641, 648, 649, 652, 653, 654, 656, 657, 658, 661, 663, 667, 669, 670, 671, 674, 676, 680, 681, 684, 688, 693, 696, 697, 698, 701, 702, 709, 710, 712, 713, 715, 720, 724, 729, 731, 733, 734, 735, 737, 738, 739, 740, 741, 742, 746, 748, 749, 754, 756, 758, 759, 760, 762, 763, 765, 766, 767, 769, 773, 776, 777, 779, 784, 786, 793, 795, 798, 799, 801, 802, 803, 804, 806, 808, 809, 811, 813, 815, 817, 819, 821, 827, 829, 833, 834, 838, 839, 840, 841, 842, 843, 844, 846, 847, 848, 851, 853, 854, 855, 856, 858, 859, 860, 861, 862, 864, 867, 868, 869, 873, 874, 875, 876, 877, 880, 881, 882, 883, 884, 885, 886, 887, 889, 891, 892, 893, 895, 901, 904, 909, 910, 911, 914, 919, 920, 921, 924, 925, 927, 929, 931, 932, 934, 935, 936, 937, 938, 939, 940, 942, 946, 947, 948, 954, 955, 956, 958, 959, 960, 962, 966, 969, 973, 976, 977, 978, 979, 980, 985, 987, 988, 989, 990, 991, 992, 993, 997, 998, 999, 1000, 1001, 1002, 1005, 1006, 1008, 1009, 1012, 1013, 1014, 1015, 1017, 1019, 1020, 1022, 1028, 1029, 1031, 1033, 1034, 1035, 1037, 1038, 1039, 1040, 1043, 1046, 1047, 1049, 1052, 1053, 1058, 1060, 1062, 1063, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1075, 1076, 1078, 1079, 1081, 1083, 1084, 1086, 1088, 1090, 1094, 1096, 1101, 1102, 1106, 1109, 1115, 1118, 1119, 1120, 1123, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1137, 1138, 1139, 1140, 1144, 1145, 1150, 1152, 1153, 1155, 1157, 1159, 1161, 1162, 1163, 1166, 1168, 1172, 1174, 1177, 1180, 1181, 1185, 1186, 1190, 1191, 1192, 1194, 1195, 1196, 1197, 1198, 1199, 1201, 1204, 1205, 1207, 1208, 1211, 1212, 1219, 1223, 1224,

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38 Human herpesvirus 6 2, 5, 8, 9, 17, 23, 26, 46, 48, 50, 60, 61, 72, 77, 88, 93, 97, 105, 112, 118, 122, 132, 133, 141, 148, 152, 164, 167, 178, 182, 183, 185, 191, 192, 196, 199, 202, 212, 220, 223, 232, 233, 243, 252, 260, 264, 275, 279, 287, 290, 296, 297, 302, 303, 315, 317, 343, 352, 355, 357, 360, 361, 362, 373, 378, 380, 383, 384, 386, 403, 404, 407, 409, 419, 423, 438, 441, 442, 447, 449, 450, 451, 455, 456, 464, 466, 469, 470, 487, 489, 490, 493, 494, 499, 505, 508, 520, 522, 525, 532, 537, 544, 545, 557, 560, 561, 562, 585, 589, 595, 599, 623, 626, 628, 632, 649, 661, 670, 695, 696, 697, 698, 706, 713, 714, 716, 718, 720, 721, 728, 733, 736, 739, 740, 744, 752, 760, 769, 774, 781, 785, 786, 805, 808, 829, 831, 839, 846, 847, 852, 854, 855, 873, 876, 892, 896, 911, 921, 929, 932, 933, 935, 937, 946, 956, 957, 958, 964, 968, 979, 982, 991, 997, 1009, 1015, 1023, 1028, 1029, 1030, 1040, 1047, 1052, 1062, 1065, 1069, 1073, 1094, 1103, 1104, 1105, 1109, 1110, 1121, 1124, 1128, 1138, 1153, 1154, 1157, 1170, 1172, 1184, 1192, 1194, 1195, 1201, 1205, 1209, 1214, 1219, 1221, 1222, 1230, 1231, 1239, 1241, 1249, 1265, 1269, 1272, 1275, 1282, 1284, 1292, 1294, 1311, 1328, 1330, 1331, 1332, 1333, 1334, 1335, 1337, 1338, 1342, 1344, 1356, 1359, 1360, 1363, 1368, 1378, 1385, 1392, 1396, 1401, 1403, 1404, 1407, 1413, 1416, 1427, 1431, 1434, 1435, 1436, 1439, 1444, 1448, 1460, 1462, 1464, 1467, 1474, 1482, 1492, 1495, 1496, 1497, 1504, 1523, 1526, 1536, 1537, 1540, 1551, 1555, 1558, 1560, 1563, 1567, 1571, 1577, 1588, 1589, 1593, 1594, 1597, 1604, 1628, 1634, 1636, 1638, 1644, 1659 and 565504-567893.

39 Human herpesvirus 6B 1, 4, 5, 8, 9, 17, 18, 19, 20, 23, 26, 29, 40, 46, 48, 50, 54, 61, 88, 93, 95, 99, 100, 122, 124, 132, 134, 141, 143, 145, 150, 152, 161, 165, 176, 196, 201, 226, 231, 233, 240, 242, 250, 264, 277, 289, 290, 292, 296, 297, 300, 302, 310, 315, 316, 320, 321, 340, 343, 347, 349, 355, 362, 365, 369, 370, 375, 378, 380, 384, 388, 403, 406, 407, 418, 423, 424, 429, 439, 447, 450, 466, 469, 472, 473, 485, 487, 489, 490, 493, 496, 501, 502, 503, 505, 510, 517, 520, 522, 525, 528, 529, 530, 532, 533, 537, 542, 550, 552, 553, 560, 563, 566, 575, 577, 579, 599, 602, 614, 615, 620, 626, 628, 633, 652, 677, 678, 685, 695, 703, 706, 710, 712, 721, 722, 724, 725, 728, 735, 737, 740, 765, 769, 774, 777, 782, 783, 786, 790, 793, 801, 803, 805, 808, 810, 821, 826, 831, 846, 850, 854, 861, 863, 873, 874, 876, 883, 886, 890, 892, 918, 924, 932, 933, 934, 937, 939, 941, 944, 946, 949, 957, 958, 962, 968, 974, 975, 977, 980, 987, 992, 993, 997, 999, 1001, 1009,

1012, 1014, 1015, 1025, 1032, 1047, 1051, 1053, 1059, 1065, 1066, 1069, 1072, 1076, 1081, 1091, 1094, 1103, 1105, 1110, 1121, 1127, 1138, 1152, 1155, 1157, 1166, 1172, 1179, 1195, 1197, 1199, 1201, 1205, 1207, 1214, 1219, 1222, 1227, 1228, 1230, 1231, 1239, 1245, 1270, 1272, 1281, 1285, 1292, 1295, 1297, 1303, 1307, 1309, 1311, 1315, 1320, 1321, 1324, 1328, 1331, 1334, 1340, 1342, 1344, 1352, 1355, 1358, 1362, 1363, 1366, 1378, 1385, 1391, 1396, 1403, 1407, 1413, 1415, 1416, 1426, 1431, 1433, 1435, 1439, 1444, 1447, 1451, 1462, 1467, 1473, 1478, 1480, 1485, 1495, 1497, 1509, 1518, 1526, 1530, 1535, 1545, 1547, 1551, 1554, 1559, 1577, 1578, 1580, 1585, 1589, 1591, 1594, 1596, 1597, 1608, 1619, 1626, 1628, 1634, 1638, 1643, 1644, 1650, 1653, 1657, 1660, 1661, 1669 and 567894-570313.

40 Human herpesvirus 7 4, 5, 7, 8, 9, 10, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 28, 29, 31, 36, 37, 40, 42, 47, 48, 49, 50, 51, 56, 60, 61, 62, 63, 67, 68, 70, 72, 73, 74, 77, 78, 86, 88, 89, 96, 97, 101, 105, 106, 109, 112, 114, 116, 120, 122, 127, 130, 132, 133, 134, 140, 141, 143, 144, 150, 151, 154, 158, 159, 162, 163, 166, 169, 171, 173, 174, 177, 179, 180, 183, 187, 188, 189, 190, 191, 196, 197, 199, 200, 201, 202, 203, 204, 207, 210, 211, 212, 218, 221, 222, 226, 231, 232, 233, 235, 236, 237, 239, 240, 241, 244, 246, 247, 248, 249, 252, 253, 262, 265, 266, 267, 269, 271, 276, 277, 279, 280, 281, 285, 286, 288, 290, 293, 296, 298, 299, 302, 303, 304, 306, 308, 310, 314, 315, 316, 319, 321, 323, 325, 328, 332, 334, 339, 342, 345, 347, 348, 350, 356, 357, 358, 359, 360, 361, 366, 367, 368, 369, 370, 374, 376, 378, 380, 382, 388, 389, 391, 393, 394, 397, 399, 400, 401, 404, 407, 408, 409, 413, 424, 426, 427, 429, 431, 433, 442, 443, 444, 446, 447, 450, 452, 453, 454, 460, 462, 463, 466, 470, 475, 478, 481, 482, 484, 485, 486, 488, 489, 500, 502, 503, 506, 507, 508, 509, 510, 512, 515, 516, 517, 518, 519, 520, 522, 523, 525, 526, 536, 537, 538, 541, 544, 546, 549, 551, 553, 557, 559, 561, 563, 564, 567, 571, 575, 576, 577, 579, 580, 583, 585, 586, 587, 592, 602, 607, 608, 610, 611, 612, 617, 620, 621, 624, 626, 627, 631, 633, 634, 635, 636, 637, 638, 639, 640, 641, 643, 645, 646, 649, 651, 652, 654, 656, 657, 659, 661, 663, 667, 670, 671, 673, 676, 681, 682, 684, 686, 688, 689, 691, 692, 693, 694, 701, 703, 707, 709, 710, 712, 713, 714, 715, 716, 717, 720, 724, 729, 731, 734, 737, 739, 742, 744, 746, 749, 750, 751, 753, 754, 758, 760, 761, 764, 765, 766, 767, 769, 771, 777, 779, 780, 781, 784, 786, 790, 793, 795, 801, 802, 803, 805, 808, 810, 812, 813, 817, 820, 821, 827, 829, 830, 836, 838, 839, 842, 846, 847, 854, 855, 856, 858, 860, 861, 862, 864, 867, 873, 875, 876, 877, 879, 881, 882, 883, 884, 886, 888, 889, 891, 894, 898, 899, 900, 901, 903, 905, 907, 909, 911, 913, 914, 920, 924, 927, 929, 931, 935, 938, 947, 953, 954, 959, 960, 961, 962, 965, 966, 971, 973, 975, 977, 980, 982, 983, 985, 988, 991, 992, 996, 997, 1002, 1004, 1005, 1006, 1007, 1008, 1009, 1013, 1015, 1016, 1017, 1019, 1020, 1021, 1022, 1024, 1028, 1029, 1031, 1036, 1038, 1039, 1041, 1046, 1049, 1050, 1058, 1060, 1062, 1063, 1065, 1069, 1070, 1071, 1074, 1076, 1078, 1083, 1086, 1092, 1094, 1095, 1099, 1101, 1103, 1106, 1108, 1109, 1110, 1111, 1114, 1118, 1120, 1122, 1123, 1126, 1127, 1128, 1129, 1131, 1133, 1134, 1135, 1138, 1139, 1140, 1141, 1144, 1146, 1152, 1153, 1154, 1156, 1157, 1159, 1163, 1166, 1168, 1172, 1173, 1174, 1175, 1181, 1182, 1184, 1185, 1186, 1187, 1190, 1191, 1194, 1195, 1196, 1197, 1198, 1199, 1202, 1204, 1205, 1206, 1207, 1211, 1212, 1214, 1215, 1218, 1219, 1220, 1221, 1222, 1225, 1226, 1227, 1230, 1233, 1235, 1237, 1243, 1248, 1249, 1251, 1252, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1266, 1267, 1268, 1270, 1271, 1272, 1275, 1277, 1279, 1280, 1282, 1283, 1284, 1285, 1288, 1289, 1293, 1295, 1296, 1297, 1299, 1300, 1303, 1305, 1310, 1311, 1312, 1314,

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- 41 Human herpesvirus 9 6, 9, 24, 40, 47, 68, 78, 128, 130, 150, 174, 177, 221, 223, 234, 247, 248, 271, 272, 279, 304, 306, 328, 334, 336, 345, 356, 370, 380, 384, 394, 403, 429, 431, 437, 466, 467, 478, 512, 537, 553, 561, 564, 575, 577, 590, 596, 598, 601, 619, 643, 688, 691, 713, 731, 770, 779, 803, 822, 823, 827, 836, 847, 855, 879, 881, 909, 931, 935, 945, 979, 993, 998, 1006, 1031, 1047, 1068, 1078, 1106, 1117, 1118, 1129, 1133, 1139, 1161, 1173, 1178, 1186, 1195, 1198, 1249, 1250, 1251, 1261, 1273, 1302, 1304, 1326, 1328, 1331, 1333, 1335, 1338, 1339, 1340, 1363, 1370, 1374, 1380, 1385, 1392, 1393, 1394, 1396, 1416, 1419, 1424, 1425, 1431, 1480, 1502, 1513, 1523, 1538, 1549, 1585, 1630, 1656 and 614865-620650.
- 42 Human immunodeficiency virus 1 (HIV-1) 1154, 1195, 1292, 1298, 1353, 1391, 1405, 1411, 1489, 1504, 1546, 1632 and 620651-620770.
- 43 Human immunodeficiency virus 2 (HIV-2) 1261, 1264, 1287, 1305, 1460, 1509, 1546, 1632, 1645 and 701430-701510.
- 44 Human metapneumovirus 1, 17, 20, 29, 36, 44, 73, 77, 112, 120, 154, 161, 186, 224, 231, 240, 276, 277, 284, 286, 288, 289, 290, 310, 321, 347, 356, 361, 429, 454, 455, 463, 488, 518, 527, 529, 544, 548, 554, 566, 575, 579, 585, 616, 625, 626, 643, 652, 653, 663, 676, 694, 696, 710, 712, 737, 739, 742, 768, 793, 795, 803, 813, 826, 839, 855, 876, 890, 894, 909, 920, 925, 941, 959, 962, 980, 1015, 1028, 1029, 1062, 1079, 1091, 1092, 1094, 1101, 1118, 1139, 1140, 1143, 1144, 1163, 1168, 1170, 1173, 1187, 1190, 1195, 1206, 1208, 1218, 1233, 1241, 1244, 1250, 1258, 1274, 1282, 1292, 1293, 1297, 1310, 1315, 1321, 1325, 1335, 1340, 1344, 1359, 1426, 1442, 1469, 1471, 1473, 1482, 1485, 1505, 1562, 1568, 1580, 1583, 1585, 1586, 1592, 1599, 1624, 1642, 1664, 1669 and 782091-786807.
- 45 Human papillomavirus type 11 1222, 1277, 1320, 1331, 1335, 1513, 1515, 1551, 1637, 1644, 1661 and 786808-787035.
- 46 Human papillomavirus type 16 1239, 1331, 1671 and 787036-787200.
- 47 Human papillomavirus type 17 1152, 1195, 1271, 1323, 1363, 1402, 1416, 1486, 1506, 1598, 1636 and 787201-788364.
- 48 Human papillomavirus type 18 1362, 1376, 1422, 1454, 1466, 1489, 1521, 1558, 1559 and 788365-788549.
- 49 Human papillomavirus type 18, complete genome 10, 410, 639, 1043, 1060, 1118, 1186, 1374, 1637 and 788550-789320.
- 50 Human papillomavirus type 19 96, 101, 102, 105, 113, 122, 125, 127, 129, 134, 148, 151, 157, 159, 168, 169,

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- 51 Human papillomavirus 1, 77, 110, 145, 162, 301, 321, 511, 531, 762, 768, 783, 1081, 1219, 1366, 1374, type 31 1454, 1551 and 813755-813950.
- 52 Human papillomavirus 1, 62, 64, 165, 288, 319, 408, 430, 533, 545, 776, 843, 886, 946, 991, 999, type 45 1089, 1138, 1292, 1324, 1466, 1551, 1638 and 813951-814099.
- 53 Human papillomavirus 4, 33, 118, 165, 201, 232, 240, 321, 368, 386, 449, 476, 484, 694, 749, 824, type 5 876, 890, 946, 1091, 1124, 1155, 1225, 1316, 1320, 1331, 1337, 1359, 1366, 1426, 1448, 1588, 1627, 1637, 1650, 1669 and 814100-814228.
- 54 Human papillomavirus 17, 26, 27, 77, 90, 112, 126, 132, 224, 269, 272, 288, 297, 319, 346, 384, 404, type 6 408, 467, 496, 504, 578, 682, 716, 749, 774, 831, 847, 924, 949, 1187, 1221, 1273, 1277, 1335, 1396, 1551, 1661 and 814229-814460.
- 55 Human papillomavirus 33, 73, 98, 118, 134, 228, 297, 311, 321, 334, 545, 739, 844, 977, 1110, 1153, type 8 1154, 1374, 1423, 1570 and 814461-814585.
- 56 Human parainfluenza 36, 98, 120, 132, 219, 231, 276, 284, 286, 288, 290, 347, 356, 360, 408, 438, virus 1 strain Washi 454, 463, 488, 522, 544, 548, 566, 579, 585, 602, 616, 620, 625, 633, 643, 653, ngton/1964 663, 676, 685, 694, 785, 793, 810, 813, 839, 855, 894, 903, 909, 910, 920, 951, 974, 980, 1011, 1025, 1029, 1036, 1062, 1076, 1079, 1084, 1092, 1101, 1109, 1118, 1139, 1140, 1144, 1163, 1168, 1173, 1187, 1190, 1195, 1207, 1208, 1222, 1258, 1281, 1293, 1315, 1325, 1335, 1368, 1442, 1469, 1471, 1482, 1505, 1545, 1554, 1562, 1578, 1585, 1586, 1624, 1631, 1642, 1650, 1653 and 814586-819257.
- 57 Human parainfluenza 36, 120, 223, 231, 276, 284, 286, 290, 347, 356, 360, 384, 404, 454, 455, 463, virus 2 488, 508, 544, 548, 563, 566, 579, 585, 616, 625, 637, 643, 653, 658, 663, 676,

- 694, 725, 739, 813, 839, 844, 855, 894, 909, 920, 958, 980, 1029, 1062, 1079, 1092, 1101, 1109, 1118, 1139, 1140, 1144, 1163, 1168, 1173, 1187, 1190, 1195, 1208, 1258, 1275, 1293, 1315, 1325, 1335, 1344, 1442, 1469, 1471, 1505, 1562, 1567, 1585, 1586, 1642 and 819258-823843.
- 58 Human parainfluenza virus 3 26, 36, 48, 60, 120, 132, 201, 231, 237, 276, 284, 286, 289, 290, 310, 347, 356, 454, 455, 463, 473, 476, 488, 544, 548, 566, 579, 585, 616, 620, 625, 626, 643, 653, 663, 676, 694, 714, 813, 839, 846, 855, 888, 894, 900, 909, 920, 958, 980, 1015, 1029, 1062, 1079, 1092, 1094, 1101, 1113, 1118, 1126, 1139, 1140, 1144, 1154, 1163, 1168, 1170, 1173, 1187, 1190, 1195, 1208, 1222, 1258, 1293, 1315, 1325, 1331, 1335, 1340, 1442, 1469, 1471, 1482, 1505, 1555, 1562, 1585, 1586, 1626, 1638, 1642, 1657 and 823844-828574.
- 59 Human parechovirus 2 4, 11, 20, 23, 24, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77, 78, 96, 114, 120, 143, 148, 169, 171, 174, 187, 188, 189, 197, 200, 203, 212, 219, 234, 239, 240, 247, 252, 261, 262, 276, 277, 279, 289, 290, 295, 303, 304, 310, 315, 321, 323, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 450, 453, 454, 462, 465, 466, 481, 484, 488, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 548, 551, 553, 561, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 616, 617, 624, 625, 627, 635, 640, 643, 652, 654, 661, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 855, 856, 862, 868, 873, 876, 882, 886, 889, 894, 909, 911, 914, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 985, 988, 998, 1006, 1008, 1019, 1020, 1029, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1069, 1070, 1079, 1084, 1086, 1090, 1092, 1096, 1101, 1106, 1118, 1123, 1129, 1133, 1138, 1139, 1140, 1152, 1153, 1159, 1163, 1168, 1172, 1173, 1187, 1190, 1195, 1196, 1198, 1204, 1205, 1208, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1315, 1321, 1325, 1328, 1330, 1332, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1442, 1456, 1459, 1467, 1469, 1471, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1507, 1511, 1526, 1549, 1552, 1557, 1574, 1578, 1579, 1580, 1584, 1585, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1642, 1643, 1654, 1656, 1665, 1669 and 828575-848188.
- 60 Human respiratory syncytial virus 5, 36, 61, 67, 96, 109, 120, 131, 132, 173, 231, 233, 263, 276, 284, 286, 290, 291, 302, 310, 316, 319, 321, 325, 332, 347, 350, 356, 359, 361, 367, 378, 382, 399, 403, 412, 426, 430, 433, 454, 455, 462, 463, 465, 466, 473, 488, 544, 548, 553, 559, 566, 567, 579, 585, 616, 625, 626, 627, 643, 653, 663, 676, 694, 701, 716, 746, 765, 785, 792, 813, 820, 826, 839, 855, 873, 887, 894, 909, 912, 920, 938, 947, 974, 980, 991, 1002, 1003, 1028, 1029, 1038, 1047, 1052, 1058, 1062, 1078, 1079, 1081, 1092, 1101, 1105, 1118, 1135, 1139, 1140, 1144, 1152, 1163, 1166, 1168, 1170, 1171, 1173, 1184, 1185, 1187, 1190, 1195, 1208, 1220, 1222, 1227, 1258, 1293, 1310, 1315, 1325, 1326, 1328, 1335, 1412, 1423, 1442, 1465, 1469, 1471, 1482, 1505, 1509, 1511, 1522, 1562, 1585, 1586, 1588, 1589, 1599, 1635, 1642 and 848189-856593.
- 61 Human rhinovirus 89 36, 120, 231, 276, 284, 286, 290, 347, 356, 454, 463, 488, 544, 548, 566, 579, 585, 616, 625, 643, 653, 663, 676, 694, 813, 839, 855, 876, 894, 909, 920, 980, 1029, 1062, 1079, 1092, 1101, 1118, 1139, 1140, 1144, 1163, 1168, 1173, 1187, 1190, 1195, 1208, 1258, 1293, 1315, 1325, 1332, 1335, 1442, 1469, 1471, 1505, 1557, 1585, 1586, 1642 and 856594-862881.
- 62 Human rhinovirus B 36, 120, 231, 276, 284, 286, 290, 347, 356, 454, 463, 488, 544, 548, 566, 579,

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63 Human T-lymphotropic 2, 5, 6, 8, 9, 10, 11, 13, 15, 19, 20, 22, 23, 24, 25, 27, 29, 31, 32, 33, 35,
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64 Human T-lymphotropic 9, 19, 26, 51, 58, 91, 102, 124, 148, 153, 174, 192, 196, 200, 203, 218, 223, virus 2

276, 290, 292, 296, 302, 316, 340, 345, 349, 369, 380, 382, 404, 421, 426, 432, 437, 444, 447, 456, 459, 466, 477, 480, 485, 504, 525, 526, 530, 545, 548, 553, 554, 571, 586, 591, 602, 625, 654, 692, 719, 750, 779, 785, 790, 793, 798, 802, 805, 813, 824, 825, 834, 850, 851, 862, 872, 879, 883, 903, 952, 973, 978, 993, 997, 999, 1022, 1029, 1035, 1036, 1042, 1059, 1063, 1067, 1069, 1072, 1075, 1077, 1083, 1084, 1094, 1108, 1133, 1139, 1143, 1146, 1197, 1201, 1204, 1208, 1222, 1224, 1250, 1253, 1265, 1279, 1287, 1298, 1300, 1301, 1303, 1316, 1333, 1336, 1348, 1353, 1359, 1363, 1365, 1373, 1419, 1427, 1430, 1436, 1444, 1486, 1499, 1504, 1511, 1537, 1545, 1560, 1561, 1566, 1579, 1585, 1588, 1589, 1610, 1636, 1637, 1647, 1650, 1651, 1668 and 930395-933934.

65 Influenza A virus 4, 7, 11, 20, 23, 24, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 66, 67, 68, 70,

73, 74, 77, 78, 96, 114, 120, 122, 133, 143, 148, 154, 169, 171, 174, 187, 188, 189, 190, 200, 203, 207, 212, 219, 221, 231, 234, 239, 240, 247, 252, 253, 257, 261, 262, 263, 266, 276, 277, 279, 284, 286, 289, 290, 291, 295, 303, 304, 310, 315, 321, 323, 325, 332, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 463, 465, 466, 481, 484, 488, 500, 507, 509, 510, 512, 515, 518, 523, 526, 537, 541, 544, 547, 548, 551, 553, 555, 559, 561, 566, 567, 574, 575, 577, 579, 585, 587, 594, 605, 607, 610, 612, 616, 617, 624, 625, 627, 635, 640, 643, 646, 652, 653, 654, 661, 663, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 781, 785, 786, 792, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 855, 856, 862, 868, 873, 876, 881, 882, 884, 886, 889, 894, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1010, 1019, 1020, 1029, 1037, 1038, 1040, 1047, 1049, 1058, 1062, 1065, 1069, 1070, 1078, 1079, 1084, 1086, 1090, 1092, 1096, 1101, 1105, 1106, 1118, 1123, 1126, 1129, 1133, 1138, 1139, 1140, 1144, 1152, 1153, 1159, 1163, 1168, 1171, 1172, 1173, 1187, 1190, 1195, 1196, 1204, 1205, 1208, 1210, 1212, 1218, 1219, 1225, 1233, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1265, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1312, 1315, 1318, 1321, 1325, 1326, 1328, 1330, 1332, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1429, 1432, 1442, 1456, 1459, 1465, 1467, 1469, 1471, 1473, 1476, 1481, 1484, 1485, 1487, 1488, 1503, 1505, 1507, 1511, 1526, 1538, 1543, 1549, 1552, 1562, 1574, 1578, 1579, 1580, 1584, 1585, 1586, 1589, 1606, 1617, 1631, 1633, 1635, 1636, 1637, 1639, 1640, 1642, 1643, 1653, 1654, 1656, 1663, 1665, 1669 and 933935-955071.

66 Influenza B virus 4, 7, 11, 20, 23, 24, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 66, 67, 68, 70,

73, 74, 77, 78, 96, 114, 120, 122, 133, 143, 148, 154, 169, 171, 174, 187, 188,

189, 190, 200, 203, 207, 212, 219, 221, 231, 234, 239, 240, 247, 252, 253, 257, 261, 262, 263, 266, 276, 277, 279, 284, 286, 289, 290, 291, 295, 303, 304, 310, 315, 321, 323, 325, 332, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 463, 465, 466, 481, 484, 488, 500, 507, 509, 510, 512, 515, 518, 523, 526, 537, 541, 544, 547, 548, 551, 553, 555, 559, 561, 566, 567, 574, 575, 577, 579, 585, 587, 594, 605, 607, 610, 612, 616, 617, 624, 625, 627, 635, 640, 643, 646, 652, 653, 654, 661, 663, 667, 676, 681, 684, 694, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 781, 785, 786, 792, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 855, 856, 862, 868, 873, 876, 881, 882, 884, 886, 889, 894, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 980, 985, 988, 998, 1006, 1008, 1010, 1019, 1020, 1029, 1037, 1038, 1040, 1047, 1049, 1058, 1062, 1065, 1069, 1070, 1078, 1079, 1084, 1086, 1090, 1092, 1096, 1101, 1105, 1106, 1118, 1123, 1126, 1129, 1133, 1138, 1139, 1140, 1144, 1152, 1153, 1159, 1163, 1168, 1171, 1172, 1173, 1187, 1190, 1195, 1196, 1204, 1205, 1208, 1210, 1212, 1218, 1219, 1225, 1233, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1265, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1312, 1315, 1318, 1321, 1325, 1326, 1328, 1330, 1332, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1429, 1432, 1442, 1456, 1459, 1465, 1467, 1469, 1471, 1473, 1476, 1481, 1484, 1485, 1487, 1488, 1503, 1505, 1507, 1511, 1526, 1538, 1543, 1549, 1552, 1562, 1574, 1578, 1579, 1580, 1584, 1585, 1586, 1589, 1606, 1617, 1631, 1633, 1635, 1636, 1637, 1639, 1640, 1642, 1643, 1653, 1654, 1656, 1663, 1665, 1669 and 959226-980361.

67 Japanese encephalitis virus 4, 7, 11, 20, 23, 24, 29, 31, 35, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74,

77, 78, 96, 114, 120, 124, 143, 148, 154, 169, 171, 174, 187, 188, 189, 196, 200, 203, 207, 212, 219, 231, 234, 239, 240, 247, 252, 261, 262, 263, 265, 277, 279, 289, 290, 291, 295, 303, 304, 310, 315, 321, 323, 325, 332, 334, 336, 339, 347, 356, 357, 363, 366, 370, 374, 376, 380, 387, 388, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 465, 466, 481, 484, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 545, 547, 551, 553, 561, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 617, 624, 627, 629, 635, 640, 652, 654, 661, 667, 676, 681, 684, 701, 702, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 785, 786, 792, 801, 803, 804, 811, 813, 815, 829, 838, 839, 840, 846, 847, 854, 856, 861, 862, 868, 873, 876, 879, 882, 886, 889, 909, 911, 914, 924, 925, 927, 935, 936, 938, 954, 960, 962, 964, 966, 969, 973, 977, 979, 981, 985, 988, 998, 999, 1006, 1008, 1019, 1020, 1036, 1037, 1038, 1040, 1047, 1049, 1058, 1062, 1065, 1069, 1070, 1078, 1084, 1086, 1090, 1096, 1101, 1105, 1106, 1113, 1123, 1129, 1133, 1138, 1139, 1150, 1152, 1153, 1159, 1162, 1163, 1168, 1171, 1172, 1190, 1196, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1269, 1270, 1271, 1274, 1277, 1284, 1287, 1290, 1293, 1294, 1297, 1299, 1306, 1312, 1321, 1326, 1328, 1330, 1332, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1407, 1411, 1412, 1416, 1419, 1423, 1424, 1426, 1432, 1456, 1459, 1465, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1493, 1503, 1507, 1511, 1521, 1526, 1549, 1552, 1562, 1567, 1574, 1578, 1579, 1580, 1584, 1589, 1606, 1617, 1631, 1633, 1635, 1637, 1639, 1640, 1643, 1654, 1656, 1665, 1669 and 982439-998310.

68 JC virus 36, 40, 50, 116, 244, 466, 529, 656, 696, 766, 817, 832, 872, 887, 971, 1050, 1129, 1483, 1523, 1640, 1642 and 998311-1001489.

- 69 Machupo virus 166, 323, 462, 478, 484, 541, 553, 559, 798, 867, 1057, 1063, 1069, 1484, 1560 and 1001490-1002112.
- 70 Marburg virus 45, 63, 64, 68, 140, 166, 169, 189, 196, 197, 201, 204, 229, 233, 237, 238, 271, 310, 316, 323, 326, 353, 366, 376, 378, 416, 448, 450, 462, 466, 478, 484, 541, 553, 557, 559, 569, 570, 614, 625, 626, 641, 656, 657, 669, 714, 720, 743, 760, 770, 798, 838, 853, 856, 859, 864, 867, 875, 887, 901, 909, 935, 954, 1002, 1005, 1015, 1029, 1047, 1057, 1063, 1069, 1094, 1134, 1138, 1185, 1186, 1195, 1198, 1199, 1205, 1222, 1239, 1276, 1285, 1299, 1308, 1328, 1340, 1344, 1351, 1358, 1372, 1373, 1386, 1400, 1402, 1406, 1484, 1488, 1508, 1545, 1560, 1611, 1623, 1638, 1642 and 1002113-1007260.
- 71 Measles virus 4, 11, 20, 21, 23, 24, 26, 29, 31, 35, 36, 37, 43, 47, 48, 49, 51, 65, 66, 67, 70, 73, 74, 77, 78, 84, 89, 96, 101, 105, 114, 120, 140, 143, 148, 154, 169, 171, 174, 183, 187, 188, 189, 197, 198, 200, 201, 203, 212, 219, 229, 231, 234, 239, 240, 247, 248, 250, 252, 253, 257, 258, 261, 262, 276, 277, 279, 284, 286, 289, 290, 292, 295, 303, 304, 306, 309, 310, 315, 321, 323, 334, 336, 339, 342, 347, 349, 350, 353, 356, 357, 363, 364, 366, 370, 374, 376, 377, 378, 380, 386, 388, 389, 394, 395, 396, 399, 400, 401, 405, 413, 415, 416, 421, 424, 429, 431, 433, 437, 441, 443, 445, 446, 450, 452, 453, 454, 462, 463, 465, 466, 475, 479, 481, 484, 485, 496, 497, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 551, 553, 559, 561, 563, 566, 567, 572, 574, 575, 577, 579, 585, 587, 594, 605, 607, 610, 612, 614, 615, 616, 617, 624, 625, 627, 635, 640, 641, 645, 646, 652, 653, 654, 658, 661, 662, 663, 667, 676, 678, 681, 684, 691, 694, 695, 701, 709, 710, 713, 715, 720, 731, 734, 737, 742, 746, 749, 754, 756, 760, 763, 765, 769, 770, 771, 773, 775, 776, 777, 779, 781, 783, 786, 801, 803, 804, 811, 813, 821, 829, 831, 838, 839, 840, 843, 846, 847, 850, 854, 856, 862, 868, 872, 873, 876, 881, 882, 884, 886, 889, 901, 909, 911, 914, 920, 924, 925, 927, 935, 936, 938, 942, 945, 950, 954, 960, 962, 966, 969, 973, 977, 978, 979, 980, 981, 985, 988, 991, 998, 1002, 1006, 1008, 1010, 1019, 1020, 1037, 1038, 1040, 1047, 1049, 1053, 1058, 1062, 1065, 1069, 1070, 1079, 1084, 1086, 1088, 1090, 1093, 1096, 1101, 1102, 1103, 1106, 1109, 1122, 1123, 1129, 1133, 1134, 1138, 1139, 1140, 1141, 1144, 1146, 1152, 1153, 1154, 1159, 1163, 1168, 1170, 1172, 1181, 1185, 1190, 1195, 1196, 1198, 1199, 1204, 1205, 1210, 1212, 1214, 1219, 1221, 1222, 1225, 1234, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1265, 1268, 1270, 1271, 1274, 1276, 1284, 1290, 1293, 1294, 1297, 1299, 1300, 1306, 1315, 1317, 1318, 1321, 1328, 1330, 1331, 1335, 1338, 1339, 1349, 1351, 1353, 1363, 1364, 1368, 1373, 1390, 1391, 1392, 1406, 1411, 1412, 1416, 1423, 1424, 1426, 1429, 1431, 1432, 1456, 1459, 1464, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1490, 1501, 1503, 1505, 1507, 1508, 1509, 1511, 1521, 1526, 1538, 1549, 1552, 1562, 1567, 1574, 1578, 1579, 1580, 1584, 1585, 1586, 1606, 1611, 1617, 1619, 1631, 1633, 1636, 1637, 1639, 1640, 1642, 1643, 1648, 1654, 1656, 1665, 1669 and 1007261-1027883.
- 72 Molluscum contagiosum virus 1, 4, 7, 12, 18, 20, 23, 26, 27, 32, 33, 35, 41, 43, 44, 46, 51, 53, 54, 58, 59, 61, 69, 72, 73, 74, 77, 81, 84, 89, 90, 93, 95, 97, 99, 100, 103, 107, 111, 115, 117, 119, 121, 123, 125, 128, 129, 134, 137, 140, 141, 143, 144, 148, 149, 151, 152, 155, 161, 162, 164, 165, 167, 173, 174, 176, 181, 182, 183, 184, 186, 191, 192, 194, 198, 202, 203, 206, 207, 211, 212, 216, 217, 218, 219, 220, 224, 225, 227, 228, 230, 231, 232, 233, 240, 245, 247, 248, 252, 253, 255, 256, 257, 258, 259, 260, 264, 265, 267, 268, 269, 274, 275, 277, 282, 283, 286, 287, 288, 290, 291, 292, 297, 300, 302, 303, 306, 307, 310, 311, 313, 314, 316, 318, 319, 321, 322, 323, 324, 326, 327, 329, 332, 334, 340, 343, 345, 346, 351, 354, 355, 357,

360, 361, 362, 365, 370, 373, 377, 380, 381, 382, 384, 385, 386, 387, 397, 401, 402, 403, 405, 406, 407, 409, 411, 415, 416, 418, 419, 423, 424, 429, 432, 434, 437, 438, 439, 441, 445, 447, 457, 464, 469, 470, 472, 473, 478, 480, 481, 483, 485, 486, 489, 490, 492, 493, 495, 496, 499, 501, 503, 504, 511, 512, 513, 514, 522, 523, 524, 529, 530, 532, 533, 535, 540, 541, 542, 543, 544, 550, 553, 559, 562, 566, 572, 574, 575, 582, 584, 586, 587, 589, 591, 594, 595, 600, 601, 605, 613, 614, 615, 616, 618, 626, 630, 632, 637, 642, 643, 648, 650, 658, 660, 661, 667, 670, 677, 678, 679, 682, 694, 695, 696, 697, 699, 710, 712, 714, 718, 719, 720, 723, 724, 728, 732, 733, 736, 738, 741, 746, 750, 755, 759, 760, 765, 768, 771, 776, 777, 778, 779, 783, 785, 790, 792, 793, 798, 799, 800, 801, 803, 804, 805, 809, 812, 813, 815, 819, 839, 840, 843, 845, 848, 850, 852, 855, 856, 864, 869, 872, 874, 876, 879, 880, 882, 883, 886, 890, 892, 893, 895, 897, 900, 901, 911, 916, 921, 924, 925, 927, 929, 932, 933, 935, 939, 940, 941, 942, 944, 948, 949, 951, 956, 957, 958, 959, 960, 962, 974, 975, 976, 977, 978, 980, 981, 991, 992, 993, 997, 999, 1001, 1004, 1008, 1012, 1014, 1015, 1017, 1018, 1023, 1026, 1028, 1029, 1032, 1033, 1035, 1038, 1039, 1040, 1043, 1047, 1049, 1062, 1067, 1069, 1072, 1075, 1076, 1077, 1079, 1083, 1088, 1089, 1091, 1093, 1098, 1102, 1109, 1115, 1118, 1120, 1121, 1126, 1128, 1129, 1131, 1133, 1136, 1137, 1139, 1152, 1153, 1154, 1155, 1163, 1167, 1170, 1177, 1179, 1181, 1185, 1187, 1191, 1192, 1194, 1197, 1201, 1205, 1206, 1207, 1209, 1215, 1218, 1219, 1222, 1223, 1224, 1225, 1226, 1227, 1230, 1233, 1239, 1240, 1245, 1249, 1253, 1254, 1255, 1258, 1263, 1264, 1268, 1273, 1277, 1281, 1284, 1287, 1289, 1291, 1292, 1294, 1300, 1301, 1303, 1307, 1310, 1316, 1317, 1318, 1320, 1321, 1324, 1327, 1328, 1330, 1331, 1333, 1334, 1336, 1337, 1340, 1341, 1342, 1345, 1346, 1348, 1352, 1355, 1356, 1358, 1359, 1360, 1363, 1366, 1367, 1370, 1375, 1378, 1382, 1387, 1389, 1391, 1396, 1399, 1405, 1406, 1408, 1410, 1411, 1412, 1414, 1416, 1420, 1421, 1422, 1423, 1426, 1433, 1435, 1436, 1438, 1439, 1442, 1443, 1444, 1447, 1448, 1454, 1455, 1458, 1459, 1462, 1466, 1467, 1469, 1472, 1473, 1474, 1480, 1481, 1482, 1485, 1490, 1492, 1498, 1499, 1504, 1508, 1514, 1515, 1518, 1519, 1528, 1529, 1530, 1533, 1535, 1537, 1538, 1541, 1546, 1551, 1555, 1559, 1572, 1575, 1577, 1580, 1581, 1582, 1583, 1591, 1592, 1597, 1598, 1600, 1604, 1609, 1624, 1628, 1631, 1634, 1636, 1638, 1642, 1643, 1644, 1647, 1648, 1650, 1651, 1652, 1653, 1654, 1664, 1665, 1667, 1668, 1669, 1671 and 1027884-1030599.

73 Murray Valley enceph 4, 11, 20, 23, 24, 29, 31, 35, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77, alitis virus 78, 90, 96, 114, 120, 143, 148, 169, 171, 174, 176, 187, 188, 189, 196, 200, 203, 212, 219, 234, 239, 240, 247, 252, 261, 262, 277, 279, 289, 290, 295, 303, 304, 310, 315, 321, 323, 325, 334, 336, 339, 347, 356, 357, 363, 366, 370, 374, 376, 380, 387, 388, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 465, 466, 481, 484, 500, 507, 509, 510, 515, 518, 526, 528, 537, 541, 544, 545, 547, 551, 553, 561, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 617, 624, 627, 635, 640, 652, 654, 661, 667, 676, 681, 684, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 856, 862, 868, 873, 876, 879, 882, 886, 889, 909, 911, 914, 924, 925, 927, 935, 936, 938, 954, 960, 962, 964, 966, 969, 973, 977, 979, 985, 987, 988, 998, 999, 1006, 1008, 1019, 1020, 1022, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1069, 1070, 1084, 1086, 1090, 1096, 1101, 1106, 1123, 1129, 1133, 1138, 1139, 1152, 1153, 1159, 1162, 1163, 1168, 1172, 1190, 1196, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1321, 1328, 1330, 1335, 1338, 1339, 1349,

- 1353, 1363, 1364, 1390, 1391, 1392, 1407, 1411, 1412, 1416, 1419, 1423, 1424, 1426, 1432, 1456, 1459, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1507, 1511, 1521, 1526, 1549, 1552, 1574, 1578, 1579, 1580, 1584, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1643, 1654, 1656, 1665, 1669 and 1030600-1044555.
- 74 Norwalk virus 148, 197, 299, 337, 401, 420, 430, 450, 466, 636, 781, 812, 824, 844, 883, 901, 915, 929, 937, 954, 1128, 1198, 1224, 1320, 1339, 1585, 1610 and 1044556-1045454.
- 75 Poliovirus 143, 154, 166, 207, 223, 239, 307, 383, 459, 533, 553, 583, 611, 683, 795, 827, 855, 876, 883, 914, 1126, 1140, 1194, 1212, 1258, 1305, 1312, 1324, 1332, 1333, 1363, 1497, 1557, 1636, 1651 and 1045455-1048772.
- 76 Puumala virus 63, 166, 271, 323, 462, 478, 484, 541, 553, 559, 569, 570, 798, 867, 1057, 1063, 1069, 1285, 1484, 1560 and 1048773-1049751.
- 77 Respiratory syncytia 5, 36, 61, 67, 72, 96, 109, 120, 132, 135, 201, 225, 231, 263, 269, 276, 284, I virus 286, 290, 291, 302, 316, 319, 321, 325, 327, 332, 347, 349, 350, 356, 359, 360, 364, 367, 369, 381, 382, 386, 399, 403, 404, 408, 412, 426, 430, 433, 454, 461, 462, 463, 465, 466, 470, 473, 479, 488, 502, 540, 544, 548, 553, 559, 566, 567, 579, 585, 616, 625, 627, 643, 653, 663, 676, 680, 694, 701, 712, 716, 746, 759, 765, 785, 792, 802, 813, 820, 826, 829, 831, 839, 855, 873, 887, 894, 896, 909, 920, 932, 938, 947, 958, 980, 991, 1003, 1009, 1028, 1029, 1038, 1047, 1058, 1062, 1078, 1079, 1092, 1093, 1101, 1105, 1118, 1132, 1135, 1138, 1139, 1140, 1141, 1144, 1152, 1154, 1157, 1163, 1166, 1168, 1171, 1173, 1185, 1186, 1187, 1190, 1195, 1208, 1220, 1222, 1227, 1241, 1258, 1275, 1276, 1283, 1293, 1315, 1325, 1326, 1328, 1335, 1340, 1389, 1408, 1412, 1423, 1442, 1465, 1469, 1471, 1482, 1493, 1505, 1509, 1511, 1547, 1559, 1562, 1571, 1585, 1586, 1589, 1599, 1623, 1635, 1642, 1657 and 1049752-1058276.
- 78 Reston Ebola virus (132, 310, 392, 801, 1214, 1346, 1613 and 1058277-1058330. REBOV)
- 79 Rubella virus 4, 6, 11, 13, 20, 23, 24, 29, 30, 31, 35, 36, 37, 40, 43, 47, 48, 49, 51, 57, 63, 64, 66, 67, 68, 70, 73, 74, 77, 78, 85, 86, 88, 92, 96, 105, 112, 114, 120, 128, 129, 138, 141, 143, 144, 148, 150, 154, 156, 159, 164, 166, 167, 168, 169, 171, 174, 177, 180, 184, 187, 188, 189, 192, 193, 195, 196, 200, 202, 203, 204, 206, 207, 209, 212, 216, 218, 219, 227, 229, 231, 233, 234, 238, 239, 240, 247, 252, 254, 256, 261, 262, 264, 265, 271, 272, 276, 277, 279, 284, 286, 290, 292, 293, 295, 296, 303, 304, 306, 310, 315, 319, 321, 323, 326, 329, 334, 336, 339, 340, 345, 346, 347, 356, 357, 366, 367, 370, 373, 374, 376, 380, 393, 394, 395, 396, 399, 400, 401, 405, 413, 418, 420, 424, 429, 431, 433, 437, 439, 441, 443, 446, 447, 448, 453, 454, 458, 462, 463, 465, 466, 467, 468, 478, 481, 482, 484, 485, 486, 488, 492, 500, 503, 505, 507, 509, 510, 515, 517, 518, 520, 521, 526, 532, 537, 540, 541, 544, 545, 547, 551, 553, 559, 561, 563, 564, 566, 567, 569, 570, 574, 575, 577, 578, 579, 585, 587, 589, 594, 597, 598, 600, 604, 605, 607, 610, 612, 614, 617, 619, 622, 624, 625, 627, 634, 635, 637, 640, 652, 653, 654, 656, 657, 661, 663, 667, 669, 671, 676, 680, 681, 684, 693, 695, 701, 709, 710, 713, 715, 720, 724, 727, 731, 734, 737, 740, 741, 746, 747, 748, 749, 750, 754, 758, 760, 763, 765, 766, 773, 776, 777, 779, 786, 796, 801, 803, 808, 809, 811, 813, 817, 829, 833, 838, 839, 840, 841, 846, 847, 848, 853, 854, 855, 858, 859, 861, 862, 867, 869, 873, 874, 875, 876, 877, 881, 882, 884, 886, 887, 889, 891, 901, 904, 909, 911, 914, 917, 919, 920, 924, 925, 927, 928, 935, 936, 938, 946, 947, 954, 955, 957, 959, 960, 962, 966, 968, 969, 971, 973, 977, 978, 979, 980, 985, 988, 989, 997, 998, 999, 1001, 1005, 1006, 1008, 1009, 1013, 1017, 1019, 1020, 1022, 1029, 1031, 1033, 1035, 1037, 1038, 1039, 1040, 1049, 1052, 1053,

1058, 1062, 1065, 1068, 1069, 1070, 1071, 1078, 1079, 1083, 1084, 1086, 1090, 1094, 1096, 1101, 1106, 1108, 1118, 1123, 1128, 1129, 1130, 1132, 1133, 1139, 1140, 1144, 1145, 1152, 1153, 1159, 1161, 1163, 1166, 1168, 1172, 1174, 1180, 1181, 1182, 1185, 1187, 1188, 1190, 1191, 1195, 1196, 1197, 1201, 1204, 1205, 1211, 1212, 1219, 1222, 1225, 1234, 1239, 1245, 1251, 1254, 1257, 1258, 1261, 1262, 1268, 1270, 1271, 1272, 1273, 1274, 1283, 1284, 1285, 1289, 1290, 1293, 1297, 1299, 1306, 1307, 1308, 1315, 1317, 1321, 1327, 1328, 1330, 1335, 1338, 1339, 1343, 1348, 1349, 1353, 1358, 1359, 1362, 1363, 1364, 1366, 1372, 1373, 1377, 1380, 1385, 1386, 1390, 1391, 1392, 1398, 1400, 1402, 1403, 1406, 1410, 1411, 1412, 1423, 1424, 1425, 1426, 1427, 1428, 1432, 1436, 1437, 1442, 1444, 1445, 1456, 1457, 1459, 1460, 1466, 1467, 1469, 1473, 1476, 1477, 1481, 1485, 1486, 1487, 1488, 1492, 1495, 1505, 1507, 1508, 1509, 1511, 1513, 1520, 1521, 1523, 1526, 1527, 1541, 1544, 1547, 1549, 1553, 1566, 1569, 1574, 1578, 1579, 1580, 1582, 1585, 1586, 1594, 1597, 1600, 1606, 1607, 1611, 1612, 1616, 1617, 1618, 1625, 1631, 1633, 1634, 1636, 1637, 1639, 1640, 1642, 1643, 1649, 1654, 1656, 1665, 1667, 1669, 1670 and 1063298-1098229.

80 SARS coronavirus 36, 40, 167, 173, 197, 198, 201, 226, 231, 237, 276, 284, 286, 289, 310, 342, 347, 356, 385, 389, 418, 441, 450, 455, 463, 466, 473, 483, 504, 514, 522, 544, 554, 566, 578, 579, 585, 616, 625, 645, 648, 653, 655, 663, 676, 694, 712, 716, 744, 768, 807, 839, 844, 855, 909, 920, 939, 954, 980, 982, 1036, 1062, 1076, 1079, 1093, 1101, 1118, 1128, 1144, 1158, 1171, 1195, 1198, 1209, 1221, 1231, 1258, 1293, 1297, 1315, 1335, 1359, 1421, 1448, 1469, 1505, 1509, 1586, 1593, 1615, 1642, 1668 and 1098230-1102172.

81 Seoul virus 63, 166, 271, 323, 462, 478, 484, 541, 553, 559, 569, 570, 798, 867, 1057, 1063, 1069, 1285, 1484, 1560 and 1102173-1103153.

82 Sin Nombre virus 8, 45, 63, 166, 271, 323, 368, 462, 478, 484, 497, 541, 553, 559, 569, 570, 798, 867, 951, 1029, 1057, 1063, 1069, 1205, 1285, 1484, 1560, 1581 and 1103154-1104234.

83 Tula virus 63, 231, 271, 284, 286, 347, 356, 463, 544, 566, 569, 570, 579, 585, 653, 663, 676, 839, 909, 920, 951, 980, 1062, 1101, 1144, 1195, 1221, 1258, 1285, 1335, 1469, 1505, 1581, 1586, 1659 and 1104235-1105729.

84 Uukuniemi virus 29, 74, 140, 645, 652, 667, 716, 737, 949, 1164 and 1105730-1105756.

85 Vaccinia virus 7, 8, 40, 44, 60, 61, 72, 75, 83, 112, 123, 132, 134, 144, 151, 173, 180, 201, 226, 248, 255, 282, 289, 315, 342, 344, 349, 360, 365, 368, 378, 388, 389, 404, 415, 440, 504, 517, 530, 536, 540, 576, 620, 626, 633, 636, 637, 639, 655, 703, 714, 716, 722, 724, 737, 742, 769, 773, 790, 804, 805, 826, 846, 847, 856, 879, 900, 910, 964, 982, 990, 1004, 1015, 1017, 1029, 1074, 1081, 1083, 1094, 1110, 1133, 1138, 1154, 1157, 1158, 1195, 1199, 1221, 1222, 1223, 1241, 1242, 1255, 1270, 1274, 1275, 1276, 1311, 1328, 1344, 1349, 1366, 1419, 1431, 1435, 1455, 1482, 1513, 1522, 1545, 1547, 1566, 1571, 1593, 1599, 1613, 1638, 1661 and 1105757-1107056.

86 Variola virus 2, 7, 8, 44, 61, 132, 134, 151, 152, 164, 173, 180, 226, 237, 247, 248, 255, 342, 344, 349, 360, 365, 368, 388, 389, 404, 414, 415, 440, 455, 464, 517, 522, 525, 530, 536, 540, 576, 585, 586, 616, 626, 633, 640, 654, 655, 694, 703, 716, 724, 742, 773, 782, 786, 790, 793, 804, 808, 826, 856, 883, 896, 900, 939, 957, 958, 964, 1004, 1017, 1029, 1042, 1094, 1154, 1157, 1158, 1170, 1171, 1186, 1195, 1199, 1221, 1222, 1227, 1231, 1241, 1242, 1249, 1255, 1270, 1272, 1275, 1276, 1280, 1311, 1342, 1344, 1347, 1349, 1362, 1366, 1416, 1455, 1479, 1482, 1522, 1547, 1551, 1566, 1599, 1638 and 1107057-1108297.

87 West Nile virus 4, 11, 20, 23, 24, 29, 31, 35, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77,

78, 96, 114, 120, 143, 148, 154, 169, 171, 174, 187, 188, 189, 200, 203, 212, 219, 234, 239, 240, 247, 252, 261, 262, 277, 279, 289, 290, 295, 303, 304, 310, 315, 321, 323, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 465, 466, 481, 484, 500, 507, 509, 510, 515, 518, 526, 537, 541, 544, 547, 551, 553, 561, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 617, 624, 627, 635, 640, 652, 654, 661, 667, 676, 681, 684, 701, 709, 710, 713, 715, 720, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 856, 862, 868, 873, 876, 882, 886, 889, 909, 911, 914, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 985, 988, 998, 1006, 1008, 1019, 1020, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1069, 1070, 1084, 1086, 1090, 1096, 1101, 1106, 1123, 1129, 1133, 1138, 1139, 1152, 1153, 1159, 1163, 1168, 1172, 1190, 1196, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1321, 1328, 1330, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1456, 1459, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1507, 1511, 1526, 1549, 1552, 1574, 1578, 1579, 1580, 1584, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1643, 1654, 1656, 1665, 1669 and 1108298-1122207.

88 Western equine encephalomyelitis virus 4, 11, 20, 23, 24, 29, 31, 35, 37, 43, 47, 48, 49, 51, 66, 67, 70, 73, 74, 77, 78, 96, 114, 120, 143, 148, 154, 169, 171, 174, 187, 188, 189, 200, 203, 212,

219, 234, 239, 240, 247, 252, 261, 262, 277, 279, 289, 290, 295, 303, 304, 310, 315, 321, 323, 334, 336, 339, 347, 356, 357, 366, 370, 374, 376, 380, 394, 395, 396, 399, 400, 401, 405, 413, 416, 424, 429, 431, 433, 437, 441, 443, 446, 453, 454, 462, 465, 466, 481, 484, 500, 507, 509, 510, 515, 518, 526, 529, 537, 541, 544, 547, 551, 553, 561, 567, 574, 575, 577, 579, 587, 594, 605, 607, 610, 612, 617, 624, 627, 635, 640, 652, 654, 661, 667, 676, 681, 684, 701, 709, 710, 713, 715, 720, 722, 731, 734, 737, 746, 749, 754, 756, 760, 763, 773, 776, 777, 786, 801, 803, 804, 811, 813, 829, 838, 839, 840, 846, 847, 854, 856, 862, 868, 873, 876, 882, 886, 889, 909, 911, 914, 924, 925, 927, 935, 936, 938, 954, 960, 962, 966, 969, 973, 977, 979, 985, 988, 998, 1006, 1008, 1019, 1020, 1037, 1038, 1040, 1049, 1058, 1062, 1065, 1069, 1070, 1084, 1086, 1090, 1096, 1101, 1106, 1123, 1129, 1133, 1138, 1139, 1152, 1153, 1159, 1163, 1168, 1172, 1190, 1196, 1204, 1205, 1212, 1219, 1225, 1239, 1245, 1251, 1254, 1257, 1258, 1262, 1268, 1270, 1271, 1274, 1284, 1290, 1293, 1297, 1299, 1306, 1321, 1328, 1330, 1335, 1338, 1339, 1349, 1353, 1363, 1364, 1390, 1391, 1392, 1411, 1412, 1416, 1423, 1424, 1426, 1432, 1456, 1459, 1467, 1469, 1473, 1476, 1481, 1485, 1487, 1488, 1503, 1507, 1511, 1526, 1549, 1552, 1574, 1578, 1579, 1580, 1584, 1606, 1617, 1631, 1633, 1637, 1639, 1640, 1643, 1654, 1656, 1665, 1669 and 1122296-1136577.

89 Yellow fever virus 166, 323, 462, 478, 484, 541, 553, 559, 798, 867, 1057, 1063, 1069, 1484, 1560 and 1136701-1137323.

90 Zaire Ebola virus (Z 563, 637, 872, 1052, 1063, 1094, 1154, 1401, 1522, 1624 and 1137324-1137407. EBOV)

GAM PRECURSOR BINDING SEQUENCE	GAM RNA SEQ OFFSET	SOURCE SRC- ORGANISM SEQUENCE	STR TARGET SITE	TARGET SITE	TAR-REF ID
=====					
=====					
AATTCCCATACATTATTGTG CGTTCAATGGAACAGGACCA		NC_0018 6406	+	IL13 Human	NM_002188
GGACATTG					
CCCCGGCTGGTTTTGCGATT TG	02			AACA	
CTAAAATGTAATAATAAGAC					
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CGTTCAATGGAACAGGACCA		NC_0018 6406	+	IL13 Human	NM_002188
GGACCTGA					
CCCCGGCTGGTTTTGCGATT TG	02			CTATTGAA	
CTAAAATGTAATAATAAGAC				G	
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CGTTCAATGGAACAGGACCA		NC_0018 6406	+	SERPINA7 Human	NM_000354
TGGCTAAT					
CCCCGGCTGGTTTTGCGATT TG	02			TGCACG	
CTAAAATGTAATAATAAGAC					
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CGTTCAATGGAACAGGACCA		NC_0018 6406	+	SERPINA7 Human	NM_000354
TGGGATGA					
CCCCGGCTGGTTTTGCGATT TG	02			AGATTGAA	
CTAAAATGTAATAATAAGAC				CC	
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA		NC_0018 6406	+	APOB Human	NM_000384
TATTGATA					
CCCCGGCTGGTTTTGCGATT TG	02			AAACCAT	
CTAAAATGTAATAATAAGAC					
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA		NC_0018 6406	+	APOB Human	NM_000384
TTTTGCAA					
CCCCGGCTGGTTTTGCGATT TG	02			GTAAAGA	
CTAAAATGTAATAATAAGAC				AAATCAG	
GTTCAATGGAACAGGACCAT					
GTACAAATGTCAGCACAGTA					
CAATGTACACATGGAATT					
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA		NC_0018 6406	+	FCGR3A Human	NM_000569
TAGAAGAT					

CCCCGGCTGGTTTTGCGATT TG	02	GGGAAAAC
CTAAAATGTAATAATAAGAC		CAT
GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ FCGR3A Human NM_000569
TGCAGGGA		
CCCCGGCTGGTTTTGCGATT TG	02	CTGTAAAA
CTAAAATGTAATAATAAGAC		CCAC
GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ IL6R Human NM_000565
TCTAGGGA		
CCCCGGCTGGTTTTGCGATT TG	02	AAAACCAG
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GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ IL6R Human NM_000565
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GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ IL6R Human NM_181359
TCTGAAAA		
CCCCGGCTGGTTTTGCGATT TG	02	CCAA
CTAAAATGTAATAATAAGAC		
GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ IL6R Human NM_181359
TCTTAGAA		
CCCCGGCTGGTTTTGCGATT TG	02	AAACCAC
CTAAAATGTAATAATAAGAC		
GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ TFRC Human NM_003234
TTTTAAAT		
CCCCGGCTGGTTTTGCGATT TG	02	AAAAGCAG
CTAAAATGTAATAATAAGAC		
GTTCAATGGAACAGGACCAT		
GTACAAATGTCAGCACAGTA		
CAATGTACACATGGAATT		
AATTCCCATACATTATTGTG CTGGTTTTGCGATTCTAAAA NC_0018 6406		+ TFRC Human NM_003234
TTTTAGAA		
CCCCGGCTGGTTTTGCGATT TG	02	AACAG

CTAAAATGTAATAATAAGAC
GTTCAATGGAACAGGACCAT
GTACAAATGTCAGCACAGTA
CAATGTACACATGGAATT
GGTGTAAACAAGCTGGTGTTT C GGTGTAAACAAGCTGGTGTTT NC_0018 8764 - NC_00180 Human im
NC_001802 5397 - GAACACCA
TCTCCTTTATTGGCCTCTTC TC 02 2 5105 - munodefi 9181 GCTTGTTA
TATCTTATCTGGCTCAACTG 5396 ge ciency v CAC
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]
GGTGTAAACAAGCTGGTGTTT C GGTGTAAACAAGCTGGTGTTT NC_0018 8764 - NC_00180 Human im
NC_001802 7971 - GAACACCA
TCTCCTTTATTGGCCTCTTC TC 02 2 5377 - munodefi 9181 GCTTGTTA
TATCTTATCTGGCTCAACTG 7970 ge ciency v CAC
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]
GGTGTAAACAAGCTGGTGTTT C GGTGTAAACAAGCTGGTGTTT NC_0018 8764 - NC_00180 Human im
NC_001802 8200 - GAACACCA
TCTCCTTTATTGGCCTCTTC TC 02 2 5516 - munodefi 9181 GCTTGTTA
TATCTTATCTGGCTCAACTG 8199 ge ciency v CAC
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]
GGTGTAAACAAGCTGGTGTTT C GGTGTAAACAAGCTGGTGTTT NC_0018 8764 - NC_00180 Human im
NC_001802 5857 - GAACACCA
TCTCCTTTATTGGCCTCTTC TC 02 2 5608 - munodefi 9181 GCTTGTTA
TATCTTATCTGGCTCAACTG 5856 ge ciency v CAC
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]
GGTGTAAACAAGCTGGTGTTT C GGTGTAAACAAGCTGGTGTTT NC_0018 8764 - NC_00180 Human im
NC_001802 8342 - GAACACCA
TCTCCTTTATTGGCCTCTTC TC 02 2 5771 - munodefi 9181 GCTTGTTA
TATCTTATCTGGCTCAACTG 8341 ge ciency v CAC
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]
GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - BDKRB2 Human NM_000623
GCTAAAC
TCTCCTTTATTGGCCTCTTC 02 CTGAGCTA
TATCTTATCTGGCTCAACTG GA
GTACTAGCTTGTAGCACC
GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - BDKRB2 Human NM_000623
GCTAGAAC
TCTCCTTTATTGGCCTCTTC 02 CTGGAGAG
TATCTTATCTGGCTCAACTG CTAGA
GTACTAGCTTGTAGCACC
GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - BDKRB2 Human NM_000623
GCTAGAAC
TCTCCTTTATTGGCCTCTTC 02 CTGGCAAG
TATCTTATCTGGCTCAACTG CTAGA
GTACTAGCTTGTAGCACC
GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - BDKRB2 Human NM_000623
GCTAGAAC

TCTCCTTTATTGGCCTCTTC	02		CTGTAGAG
TATCTTATCTGGCTCAACTG			CTAGA
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- BDKRB2 Human NM_000623
GCTAGAAT			
TCTCCTTTATTGGCCTCTTC	02		CTGGAGAG
TATCTTATCTGGCTCAACTG			CTAGA
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- CFTR Human NM_000492
TCTCATT			
TCTCCTTTATTGGCCTCTTC	02		CCAAGCAA
TATCTTATCTGGCTCAACTG			GTA
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- CFTR Human NM_000492
TGCCATGT			
TCTCCTTTATTGGCCTCTTC	02		GCTAGTA
TATCTTATCTGGCTCAACTG			
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- CFTR Human NM_000492
TGCCACA			
TCTCCTTTATTGGCCTCTTC	02		GCTGTA
TATCTTATCTGGCTCAACTG			
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- IL6ST Human NM_175767
TGCTACAA			
TCTCCTTTATTGGCCTCTTC	02		CTTCAGCA
TATCTTATCTGGCTCAACTG			GTA
GTTAGCTTGTAGCACC			
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- NC_00180 Human im NC_001802
4643 - GTACAAGG			
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodef	9181 AGCTTGTA
TATCTTATCTGGCTCAACTG		4642 gen ciency v	
GTTAGCTTGTAGCACC		e irus 1 [
		HIV-1]	
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- NC_00180 Human im NC_001802
4643 - TACTAATA			
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodef	9181 CCAATAGT
TATCTTATCTGGCTCAACTG		4642 gen ciency v	AGTA
GTTAGCTTGTAGCACC		e irus 1 [
		HIV-1]	
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- NC_00180 Human im NC_001802
4643 - TACTACCA			
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodef	9181 GCTATA
TATCTTATCTGGCTCAACTG		4642 gen ciency v	
GTTAGCTTGTAGCACC		e irus 1 [
		HIV-1]	
GGTGTAAACAAGCTGGTGTTT		NC_0018 8764	- NC_00180 Human im NC_001802
4643 - TCTAGCAG			
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodef	9181 AAGAAGAG
TATCTTATCTGGCTCAACTG		4642 gen ciency v	GTAGTA

GTACTAGCTTGTAGCACC		e	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
4643 - TCTATCAA				
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodefi	9181	AGCAGTA
TATCTTATCTGGCTCAACTG		4642 gen	ciency v	
GTACTAGCTTGTAGCACC		e	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
4643 - TGCCACAG				
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodefi	9181	CCATAGCA
TATCTTATCTGGCTCAACTG		4642 gen	ciency v	GTA
GTACTAGCTTGTAGCACC		e	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
4643 - TTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 336 - munodefi	9181	CAGCTGTA
TATCTTATCTGGCTCAACTG		4642 gen	ciency v	
GTACTAGCTTGTAGCACC		e	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5166 - GTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 4587 - munodefi	9181	AGCTTGTA
TATCTTATCTGGCTCAACTG		5165 ge	ciency v	
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5166 - TACTAATA				
TCTCCTTTATTGGCCTCTTC	02	2 4587 - munodefi	9181	CCAATAGT
TATCTTATCTGGCTCAACTG		5165 ge	ciency v	AGTA
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5166 - TACTACCA				
TCTCCTTTATTGGCCTCTTC	02	2 4587 - munodefi	9181	GCTATA
TATCTTATCTGGCTCAACTG		5165 ge	ciency v	
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5166 - TCTAGCAG				
TCTCCTTTATTGGCCTCTTC	02	2 4587 - munodefi	9181	AAGAAGAG
TATCTTATCTGGCTCAACTG		5165 ge	ciency v	GTAGTA
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5166 - TCTATCAA				
TCTCCTTTATTGGCCTCTTC	02	2 4587 - munodefi	9181	AGCAGTA
TATCTTATCTGGCTCAACTG		5165 ge	ciency v	
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5166 - TGCCACAG
TCTCCTTTATTGGCCTCTTC 02 2 4587 - munodefi 9181 CCATAGCA
TATCTTATCTGGCTCAACTG 5165 ge ciency v GTA
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5166 - TGCTACAA
TCTCCTTTATTGGCCTCTTC 02 2 4587 - munodefi 9181 GCTAGTA
TATCTTATCTGGCTCAACTG 5165 ge ciency v
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5166 - TTACAAGG
TCTCCTTTATTGGCCTCTTC 02 2 4587 - munodefi 9181 CAGCTGTA
TATCTTATCTGGCTCAACTG 5165 ge ciency v
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - GTACAAGG
TCTCCTTTATTGGCCTCTTC 02 2 5105 - munodefi 9181 AGCTTGTA
TATCTTATCTGGCTCAACTG 5396 ge ciency v
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - TACTAATA
TCTCCTTTATTGGCCTCTTC 02 2 5105 - munodefi 9181 CCAATAGT
TATCTTATCTGGCTCAACTG 5396 ge ciency v AGTA
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - TACTACCA
TCTCCTTTATTGGCCTCTTC 02 2 5105 - munodefi 9181 GCTATA
TATCTTATCTGGCTCAACTG 5396 ge ciency v
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - TCTAGCAG
TCTCCTTTATTGGCCTCTTC 02 2 5105 - munodefi 9181 AAGAAGAG
TATCTTATCTGGCTCAACTG 5396 ge ciency v GTAGTA
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - TCTATCAA
TCTCCTTTATTGGCCTCTTC 02 2 5105 - munodefi 9181 AGCAGTA
TATCTTATCTGGCTCAACTG 5396 ge ciency v
GTACTAGCTTGTAGCACC ne irus 1 [
HIV-1]

GGTGTAAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5397 - TGCCACAG

TCTCCTTTATTGGCCTCTTC	02	2 5105 - munodefi	9181	CCATAGCA
TATCTTATCTGGCTCAACTG		5396 ge ciency v		GTA
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
5397 - TGCTACAA				
TCTCCTTTATTGGCCTCTTC	02	2 5105 - munodefi	9181	GCTAGTA
TATCTTATCTGGCTCAACTG		5396 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
5397 - TTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5105 - munodefi	9181	CAGCTGTA
TATCTTATCTGGCTCAACTG		5396 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
7971 - GTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5377 - munodefi	9181	AGCTTGTA
TATCTTATCTGGCTCAACTG		7970 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
7971 - TGCCACAG				
TCTCCTTTATTGGCCTCTTC	02	2 5377 - munodefi	9181	CCATAGCA
TATCTTATCTGGCTCAACTG		7970 ge ciency v		GTA
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
7971 - TGCTACAA				
TCTCCTTTATTGGCCTCTTC	02	2 5377 - munodefi	9181	GCTAGTA
TATCTTATCTGGCTCAACTG		7970 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
7971 - TTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5377 - munodefi	9181	CAGCTGTA
TATCTTATCTGGCTCAACTG		7970 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
7971 - GTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5516 - munodefi	9181	AGCTTGTA
TATCTTATCTGGCTCAACTG		8199 ge ciency v		
GTACTAGCTTGTAGCACC		ne irus 1 [
HIV-1]				
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC		NC_0018 8764	-	NC_00180 Human im NC_001802
8200 - TGCCACAG				
TCTCCTTTATTGGCCTCTTC	02	2 5516 - munodefi	9181	CCATAGCA
TATCTTATCTGGCTCAACTG		8199 ge ciency v		GTA

GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
8200 - TGCTACAA				
TCTCCTTTATTGGCCTCTTC	02	2 5516 - munodefi	9181	GCTAGTA
TATCTTATCTGGCTCAACTG		8199 ge ciency v		
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
8200 - TTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5516 - munodefi	9181	CAGCTGTA
TATCTTATCTGGCTCAACTG		8199 ge ciency v		
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - GTACAAGG				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	AGCTTGTA
TATCTTATCTGGCTCAACTG		5856 ge ciency v		
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - TACTAATA				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	CCAATAGT
TATCTTATCTGGCTCAACTG		5856 ge ciency v		AGTA
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - TACTACCA				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	GCTATA
TATCTTATCTGGCTCAACTG		5856 ge ciency v		
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - TCTAGCAG				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	AAGAAGAG
TATCTTATCTGGCTCAACTG		5856 ge ciency v		GTAGTA
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - TGCCACAG				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	CCATAGCA
TATCTTATCTGGCTCAACTG		5856 ge ciency v		GTA
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			
GGTGTAAACAAGCTGGTGTTTCTACTAGCTTGTAGCACC	NC_0018 8764	-	NC_00180 Human im NC_001802	
5857 - TGCTACAA				
TCTCCTTTATTGGCCTCTTC	02	2 5608 - munodefi	9181	GCTAGTA
TATCTTATCTGGCTCAACTG		5856 ge ciency v		
GTACTAGCTTGTAGCACC		ne	irus 1 [
	HIV-1]			

GGTGTAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
5857 - TTACAAGG

TCTCCTTTATTGGCCTCTTC 02 2 5608 - munodefi 9181 CAGCTGTA
TATCTTATCTGGCTCAACTG 5856 ge ciency v
GTA TAGCTTGTAGCACC ne irus 1 [

HIV-1]

GGTGTAACAAGCTGGTGTTT TACTAGCTTGTAGCACC NC_0018 8764 - NC_00180 Human im NC_001802
8342 - TGCTACAA

TCTCCTTTATTGGCCTCTTC 02 2 5771 - munodefi 9181 GCTAGTA
TATCTTATCTGGCTCAACTG 8341 ge ciency v
GTA TAGCTTGTAGCACC ne irus 1 [

HIV-1]

GTA CTGGGTCTCTCTGGTTA GGGTCTCTCTGGTTAGACCA NC_0018 9080 + MHC2TA Human NM_000246
GGATAGAG

GACCAGATCTGAGCCTGGGA GA 02 AGAGACCA
GCTCTCTGGCTAACTAGGGA
ACCCACTGC

GTA CTGGGTCTCTCTGGTTA GGGTCTCTCTGGTTAGACCA NC_0018 9080 + MHC2TA Human NM_000246
TGGCTAGG

GACCAGATCTGAGCCTGGGA GA 02 ACCC
GCTCTCTGGCTAACTAGGGA
ACCCACTGC

GTA CTGGGTCTCTCTGGTTA GGGTCTCTCTGGTTAGACCA NC_0018 9080 + TP73 Human NM_005427
TGCGCCAC

GACCAGATCTGAGCCTGGGA GA 02 CGCCCAGA
GCTCTCTGGCTAACTAGGGA GACCC
ACCCACTGC

GTA CTGGGTCTCTCTGGTTA GGGTCTCTCTGGTTAGACCA NC_0018 9080 + VDR Human NM_000376
GGTCTAGG

GACCAGATCTGAGCCTGGGA GA 02 GAGAGACC
GCTCTCTGGCTAACTAGGGA C
ACCCACTGC

GTA CTGGGTCTCTCTGGTTA TCTGGCTAACTAGGGAACCC NC_0018 9080 + IL1A Human NM_000575
GCTTATCC

GACCAGATCTGAGCCTGGGA AC 02 CATAGCCA
GCTCTCTGGCTAACTAGGGA GG
ACCCACTGC

GTA CTGGGTCTCTCTGGTTA TCTGGCTAACTAGGGAACCC NC_0018 9080 + IL1A Human NM_000575
GGCATCCT

GACCAGATCTGAGCCTGGGA AC 02 CCACAATA
GCTCTCTGGCTAACTAGGGA GCAGA
ACCCACTGC